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JOURNAL OF BACTERIOLOGY, vol. 168, no. 2, November 1986, pages 607-612, American Society for Microbiology; K.L. PERRY et al.: "Cloning and regulation of *Erwinia herbicola* pigment genes"

J. GEN. MICROBIOL., vol. 130, 1984, pages 1623-1631, SGM; G. THIRY: "Plasmids of the epiphytic bacterium *Erwinia uredovora*"

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CHEMICAL ABSTRACTS, vol. 109, no. 17, 24th October 1988, page 172, abstract no.143512y, Columbus, Ohio, US; G. GIULIANO et al.: "A genetic-physical map of the Rhodobacter capsulatus carotenoid biosynthesis gene cluster", & MGG, MOL. GEN. GENET. 1988, 213(1), 78-83

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Description

Field of the Art

5 The present invention relates to DNA sequences which are useful for the synthesis of carotenoids such as lycopene, β -carotene, zeaxanthin or zeaxanthin-diglucoside.

The present invention also relates to processes for producing such carotenoid compounds.

Related Art

10 Carotenoids are distributed widely in green plants. They are yellow-orange-red lipids which are also present in some mold, yeast and so forth, and have recently received increased attention as natural coloring materials for foods. Among these carotenoids, β -carotene is a typical one, which is used as a coloring materials and as a precursor of vitamin A in mammals as well. It is also examined for its use as a component for preventing cancer [see, for example, SHOKUHIN TO KAIHATSU (Foods and Development), 24, 61-65 (1989)]. Carotenoids such as β -carotene are widely distributed in green plants, so that the plant tissue culture has been examined for the development of a method for producing carotenoids in a large amount which is free from the influence of natural environment [see, for example, Plant Cell Physiol., 12, 525-531 (1971)]. The examination has been also made for detecting a microorganism such as mold, yeast or green algae which is originally high carotenoid productive and for producing carotenoids in a large amount with use of such microorganism (see, for example, The Abstract of Reports in the Annual Meeting of NIPPON HAKKO KOGAKU-KAI of 1988, page 139). However, neither of these methods are successful at present in producing β -carotene at a good productivity which exceeds the synthetic method in commercial production of β -carotene. It would be very useful to obtain a gene group which participates in the biosynthesis of carotenoids, because it will be possible to produce carotenoids in a large amount by introducing a gene group which has been reconstructed to express proper genes in the gene group in a large amount, into an appropriate host such as a plant tissue culture cell, a mold, an yeast or the like which originally produces carotenoids. Such a development in technology has possibilities for finding a method of producing β -carotene superior to the synthetic method and a method of producing useful carotenoids other than β -carotene in a large amount.

Furthermore, the synthesis of carotenoids in a cell or an organ which produces no carotenoid will be possible by obtaining the gene group participating in the biosynthesis of carotenoids, which will add new values to organisms. For example, several reports have recently been made with reference to creating flower colors which cannot be found in nature by using genetic manipulation in flowering plants [see, for example, Nature, 330, 677-678 (1987)]. The color of flowers is developed by pigments such as anthocyanine or carotenoids. Anthocyanine is responsible for flower colors in the spectrum of red-violet-blue, and carotenoids are responsible for flower colors in the spectrum of yellow-orange-red. The gene of the enzyme for synthesizing anthocyanine has been elucidated, and the aforementioned reports for creating a new flower color are those referring to anthocyanine. On the other hand, there are many flowering plants having no bright yellow flower due to no function of synthesizing carotenoids in petal (e.g. petunia, saintpaulia (african violet), cyclamen, Primula malacoides, etc.). If suitable genes having been reconstructed so as to be expressed in petal in a gene group referring to the biosynthesis of carotenoids are introduced into these flowering plants, the flowering plants having yellow flowers will be created successfully.

However, enzymes for synthesizing carotenoids or genes coding for them have been scarcely elucidated at present. The nucleotide sequence of the gene group participating in the biosynthesis of a kind of carotenoids has been elucidated lately only in a photosynthetic bacterium *Rhodobacter capsulatus* [Mol. Gen. Genet., 216, 254-268 (1989)]. But this bacterium synthesizes the acyclic xanthophyll spheroidene via neurosporene without cyclization and thus cannot synthesize general carotenoids such as lycopene, β -carotene and zeaxanthin.

50 There are prior arts with reference to yellow pigments or carotenoids of *Erwinia* species disclosed in J. Bacteriol., 168, 607-612 (1986), J. Bacteriol., 170, 4675-4680 (1988) and J. Gen. Microbiol., 130, 1623-1631 (1984). The first one of these references discloses the cloning of a gene cluster coding for yellow pigment synthesis from *Erwinia herbicola* Eho 10 ATCC 39368 as a 12.4 kilobase pair (kb) fragment. In this connection, there is no illustration of the nucleotide sequence of the 12.4 kb fragment. The second literature discloses the yellow pigment synthesized by the cloned gene cluster, which is indicated to belong to carotenoids by the analysis of its UV-visible spectrum. The last literature indicates that the gene participating in the production of a yellow pigment is present in a 260 kb large plasmid contained in *Erwinia uredovora* 20D3 ATCC 19321 from the observation that the yellow pigment is not produced on curing the

large plasmid, and further discloses that the pigment belongs to carotenoids from the analysis of its UV-visible spectrum.

However, the chemical structures of carotenoids produced by the *Erwinia* species or of its metabolic intermediates, enzymes participating in the synthesis of them or the nucleotide sequence of the genes encoding these enzymes remain unknown at present.

DISCLOSURE OF THE INVENTION

The object of the present invention is to provide DNA sequences which are useful for the synthesis of carotenoids such as lycopene, β -carotene, zeaxanthin or zeaxanthin-diglucoside, that is DNA sequences encoding carotenoid biosynthesis enzymes.

In other words, the DNA sequences useful for the synthesis of carotenoids according to the present invention are the DNA sequences ① - ⑥ described in the following items (1) - (6).

(1) a DNA sequence encoding an enzyme polypeptide which participates in a step before the phytoene stage in carotenoid biosynthesis proceeding via geranylgeranyl pyrophosphate, phytoene and zeaxanthin-diglucoside and whose amino acid sequence corresponds substantially to the amino acid sequence from A to B shown in Figs. 1(a) and (b) (DNA sequence ①);

(2) a DNA sequence encoding a polypeptide which has an enzymatic activity for converting zeaxanthin into zeaxanthin-diglucoside and whose amino acid sequence corresponds substantially to the amino acid sequence from C to D shown in Figs. 2-(a) and (b) (DNA sequence ②);

(3) a DNA sequence encoding a polypeptide which has an enzymatic activity for converting lycopene into β -carotene and whose amino acid sequence corresponds substantially to the amino acid sequence from E to F shown in Figs. 3-(a) and (b) (DNA sequence ③);

(4) a DNA sequence encoding a polypeptide which has an enzymatic activity for converting phytoene into lycopene and whose amino acid sequence corresponds substantially to the amino acid sequence from G to H shown in Figs. 4-(a), (b) and (c) (DNA sequence ④);

(5) a DNA sequence encoding a polypeptide which has an enzymatic activity of converting geranylgeranyl pyrophosphate as a substrate into a next carotenoid compound in the carotenoid biosynthesis proceeding via geranylgeranyl pyrophosphate, phytoene and zeaxanthin-diglucoside and whose amino acid sequence corresponds substantially to the amino acid sequence from I to J shown in Figs. 5-(a) and (b) (DNA sequence ⑤); and

(6) a DNA sequence encoding a polypeptide which has an enzymatic activity for converting β -carotene into zeaxanthin and whose amino acid sequence corresponds substantially to the amino acid sequence from K to L shown in Fig. 6 (DNA sequence ⑥).

Another object of the present invention is to provide processes for producing carotenoid compounds.

More specifically, the present invention also provides a process for producing a carotenoid compound which is related from the group consisting of prephytoene pyrophosphate, phytoene, lycopene, β -carotene, zeaxanthin and zeaxanthin-diglucoside, which comprises transforming a host with at least one of DNA sequences ① - ⑥ described above and culturing the transformant.

Effect of the Invention

The successful acquirement of the gene group (gene group encoding the biosynthetic enzymes of carotenoids) useful for the synthesis of carotenoids such as lycopene, β -carotene, zeaxanthin, zeaxanthin-diglucoside or the like according to the present invention has made it possible to produce useful carotenoids in large amounts, for example, by creating a plasmid in which the gene(s) can be expressed in a large amount and employing an appropriate plant tissue culture cell, a microorganism or the like transformed with the plasmid. The success in acquiring the gene group useful for the synthesis of carotenoids such as lycopene, β -carotene, zeaxanthin, zeaxanthin-diglucoside or the like according to the present invention has made it possible to synthesize carotenoids in cells or organs which produce no carotenoid by creating a plasmid in which the gene(s) can be expressed in a target cell or organ and transforming a suitable host with this plasmid.

DETAILED DESCRIPTION OF THE INVENTION

The DNA sequences according to the present invention are the aforementioned DNA sequences ① - ⑥, that is, genes encoding the polypeptides of respective enzymes which participate in the biosynthesis reaction of carotenoids, in particular, for example, such polypeptides in *Erwinia uredovora* 20D3 ATCC

19321.

A variety of gene groups containing the DNA sequences of a combination of a plurality of sequences among these DNA sequences ① - ⑥ can be expressed in a microorganism, a plant or the like to afford them the biosynthesis ability of carotenoids such as lycopene, β -carotene, zeaxanthin, zeaxanthin-diglucoside or the like. The respective DNA sequences constructing the gene group may be present on a DNA strand or on different DNA strands individually, or optionally, the respective DNA sequences may comprise a plurality of DNA sequences present on a DNA strand and a DNA sequence present on another DNA strand.

The aforementioned gene group encode the polypeptides of a plurality of enzymes participating in the production of carotenoids. A recombinant DNA is created by incorporating the gene group into a proper vector and then introduced into a suitable host to create a transformant, which is cultured to produce mainly in the transformant a plurality of enzymes participating in the formation reaction of carotenoids and to conduct the biosynthesis of carotenoids in the transformant by these enzymes.

The DNA sequence shown in Fig. 7-(a) to (g), which is an example according to the present invention, is acquired from *Erwinia uredovora* 20D3 ATCC 19321 and thus exhibits, as illustrated in the experimental example below, no homology in the DNA-DNA hybridization with the DNA strand containing the gene group for synthesizing the yellow pigment of *Erwinia herbicola* Eho 10 ATCC 39368 (see Related Art described above).

DNA Sequences encoding the polypeptide of each enzyme

The DNA sequences of the present invention are the DNA sequences ① - ⑥ (or the DNA strands ① - ⑥), respectively. Each of the DNA sequences contains a nucleotide sequence encoding the polypeptide whose amino acid sequence corresponds substantially to such an amino acid sequence as in the aforementioned specific regions in Figs. 1 - 6 (for example, from A to B in Fig. 1). In this connection the term "DNA sequence" means a polydeoxyribonucleic acid sequence having a length. In the present invention, the "DNA sequence" is defined by an amino acid sequence of a polypeptide which is encoded by the DNA sequence and has a definite length as described above, so that each DNA sequence has also a definite length. However, the DNA sequence contains a gene encoding each enzyme and is useful for biotechnological production of the polypeptide, and such biotechnological production cannot be performed by only the DNA sequence having a definite length but can be performed in the state where other DNA sequence with a proper length is linked to the 5'-upstream and/or the 3'-downstream of the DNA sequence. Therefore, the term "DNA sequence" in the present invention includes, in addition to those having a definite length (for example, the length in the region of A - B in the corresponding amino acid sequence of Fig. 1), those in the form of a linear DNA strand or a circular DNA strand containing the DNA sequence having a definite length as a member.

One of the typical forms of each DNA sequence according to the present invention is a form of a plasmid which comprises the DNA sequence as a part of a member or a form in which the plasmid is present in a host such as *E. coli*. The plasmid as one of the preferable existing forms of each DNA sequence according to the present invention is a conjunction of the DNA sequence according to the present invention as a passenger or a foreign gene, a replicable plasmid vector present stably in a host and a promoter (containing ribosome-binding sites in the case of a procaryote). As the plasmid vector and the promoter, an appropriate combination of those which are well-known can be used.

Polypeptides encoded by DNA sequences

As mentioned above, the DNA sequences according to the present invention are respectively specified by the amino acid sequences of the polypeptides encoded thereby. Each of these polypeptides is the one having an amino acid sequence which corresponds substantially to an amino acid sequence in a specific region as described above in Figs. 1 - 6 (for example, from A to B in Fig. 1). Here, in the six (A-B, C-D, E-F, G-H, I-J, K-L) polypeptides shown in Figs. 1-6 (i.e. six enzymes participating in the formation of carotenoids), some of the amino acids can be deleted or substituted or some amino acids can be added or inserted, etc., so long as each polypeptide has the aforementioned enzymatic activity in the relationship of a substrate and a converted substance (a product). This is indicated by the expression "whose amino acid sequence corresponds substantially to ..." in the claims. For example, each polypeptide that first amino acid (Met) has been deleted from each polypeptide shown in Figs. 1 - 6 is included in such deleted polypeptides.

The typical polypeptides having enzymatic activities, respectively, in the present invention are those in the specific regions in Figs. 1 - 6 described above, and the amino acid sequences of these polypeptides have not been known.

5 Nucleotide sequences of DNA sequences

The DNA sequences encoding the respective enzymes are those having the nucleotide sequences in the aforementioned specific regions in Figs. 1 - 6 (for example, A-B in Fig. 1) or degenerative isomers thereof, or those having the nucleotide sequences corresponding to the aforementioned alteration of the amino acid sequence of respective enzymes or degenerative isomers thereof. The term "degenerative isomer" means DNA sequence which is different only in degenerative codon and can code for the same polypeptide. The preferred embodiments of the DNA sequences according to the present invention are those having at least one stop codon (such as TAA) at the 3'-terminal. The 5'-upstream and/or the 3'-downstream of the DNA sequences according to the present invention may further have a DNA sequence with a certain length as a non-translation region (the initial portion of the 3'-downstream being usually a stop codon such as TAA).

Gene group used for the synthesis of carotenoids

The gene group (the gene cluster in some case) used for the synthesis of carotenoids comprises a plurality of the aforementioned DNA sequences ① - ⑥, whose typical examples are illustrated in the following (1) - (4). Each gene group encodes a plurality of polypeptides of respective enzymes and these enzymes participate in the production reaction of carotenoids to produce them from their substrates.

25 (1) Gene group used for the synthesis of lycopene

The gene group used for the synthesis of lycopene which is a red carotenoid is DNA sequence comprising the aforementioned DNA sequences ①, ④ and ⑤, and such a gene group includes the one in which respective DNA sequences are present on one DNA strand or on different DNA strands separately or the one which is constructed by the combination of the aforementioned ones according to necessities.

In the case that a plurality of DNA sequences are present on one DNA strand, the arrangement order and direction of the aforementioned DNA sequences ①, ④ and ⑤ may be optional provided that the genetic information is capable of expression, that is to say respective genes in a host are in a state of being transcribed and translated appropriately.

The biosynthetic pathway of lycopene in *E. coli* is explained as follows: geranylgeranyl pyrophosphate which is a substrate originally present in *E. coli* is converted into prephytoene pyrophosphate by the enzyme encoded by the DNA sequence ⑤, the prephytoene pyrophosphate is then converted into phytoene by the enzyme encoded by the DNA sequence ①, and the phytoene is further converted into lycopene by the enzyme encoded by the DNA sequence ④ (see Fig. 8).

Lycopene is a carotene whose color is red. Lycopene is a red pigment which is present in a large amount in the fruits of water melon or tomato and has high safety for food. In this connection, the lycopene which was synthesized by the DNA sequences according to the present invention in the experimental example described below had the same stereochemistry as lycopene present in these plants.

One of the typical existing forms of the gene group of the present invention is a form of a plasmid which comprises the respective DNA sequences containing a stop codon as a member or a form in which the plasmid is present in a host such as *E. coli*. The plasmid which is one of the preferred existing forms of the gene group according to the present invention comprises a gene group as a passenger or a foreign gene, a replicable plasmid vector present stably in a host and a promoter (containing ribosome-binding sites in the case of a procaryote). As the promoter, in procaryotes such as *E. coli* or *Zymomonas* species a promoter which is common to respective DNA sequences can be used, or alternatively respective promoters can be used to the respective DNA sequences. In the case of eucaryotes such as yeast or plant, respective promoters are preferably used to respective DNA sequences.

One of the preferred existing forms of the DNA sequences are described above in the explanation of the DNA sequences ① - ⑥.

(2) Gene group used for the synthesis of β -carotene

The gene group used for the synthesis of β -carotene which is one of yellow-orange carotenoids is a DNA sequence comprising the aforementioned DNA sequences ①, ③, ④ and ⑤. In other words, the gene group used for the synthesis of β -carotene is formed by adding the DNA sequence ③ to a DNA sequence used for the synthesis of lycopene comprising the DNA sequences and ①, ④, and ⑤. The gene group includes the one in which the respective DNA sequences constructing the gene group may be present on one DNA strand or on different DNA strands individually, or the one which is constructed by the combination of the aforementioned ones according to necessities.

In the case that a plurality of DNA sequences are present on one DNA strand, the arrangement order and direction of the aforementioned DNA sequences ①, ③, ④ and ⑤ may be optional provided that the genetic information is capable of expression, that is to say respective genes in a host are in a state of being transcribed and translated appropriately.

The biosynthetic pathway of β -carotene in *E. coli* is explained as follows: geranylgeranyl pyrophosphate which is a substrate originally present in *E. coli* is converted into prephytoene pyrophosphate by the enzyme encoded by the DNA sequence ⑤, the prephytoene pyrophosphate is converted into phytoene by the enzyme encoded by the DNA sequence ①, the phytoene is further converted into lycopene by the enzyme encoded by the DNA sequence ④, and the lycopene is further converted into β -carotene by the enzyme encoded by the DNA sequence ③, (see Fig. 8).

β -carotene is a typical carotene whose color is in the spectrum ranging from yellow to orange, and it is an orange pigment which is present in a large amount in the roots of carrot or green leaves of plants and has high safety for food. The utility of β -carotene has already been described in the explanation of related art. In this connection, the β -carotene which was synthesized by the DNA sequence according to the present invention in the experimental example described below had the same stereochemistry as β -carotene present in the roots of carrot or green leaves of plants.

One of the typical existing forms of the gene group and the individual DNA sequences are the same as defined in (1).

(3) Gene group used for the synthesis of zeaxanthin

The gene group used for the synthesis of zeaxanthin which is one of yellow-orange carotenoids is a DNA sequence comprising the aforementioned DNA sequences ①, ③, ④, ⑤ and ⑥. In other words, the DNA sequence used for the synthesis of zeaxanthin is formed by adding the DNA sequence ⑥ to a DNA sequence used for the synthesis of β -carotene comprising the DNA sequences ①, ③, ④ and ⑤. The gene group includes the one in which the respective DNA sequences constructing the gene group are present on one DNA strand or on different DNA strands individually, or the one which is constructed by the combination of the aforementioned ones according to necessities.

In the case that a plurality of DNA sequences are present on one DNA strand, the arrangement order and direction of the aforementioned DNA sequences ①, ③, ④, ⑤ and ⑥ may be optional provided that the genetic information is capable of expression, that is to say respective genes in a host are in a state of being transcribed and translated appropriately.

The biosynthetic pathway of zeaxanthin in *E. coli* is explained as follows: geranylgeranyl pyrophosphate which is a substrate originally present in *E. coli* is converted into prephytoene pyrophosphate by the enzyme encoded by the DNA sequence ⑤, the prephytoene pyrophosphate is converted into phytoene by the enzyme encoded by the DNA sequence ①, the phytoene is then converted into lycopene by the enzyme encoded by the DNA sequence ④, and the lycopene is further converted into β -carotene by the enzyme encoded by the DNA sequence ③, and finally the β -carotene is converted into zeaxanthin by the enzyme encoded by the DNA sequence ⑥ (see Fig. 8).

Zeaxanthin is a xanthophyll whose color is in the spectrum ranging from yellow to orange, and it is a yellow pigment which is present in the seed of maize and has high safety for food. Zeaxanthin is contained in feeds for hen or colored carp and is an important pigment source for coloring them. In this connection, the zeaxanthin which was synthesized by the DNA sequences according to the present invention in the experimental example described below had the same stereochemistry as zeaxanthin described above.

One of the typical existing forms of the gene group and the individual DNA sequences is the same as defined in (1).

(4) Gene group used for the synthesis of zeaxanthin-diglucoside

The gene group used for the synthesis of zeaxanthin-diglucoside which is one of yellow-orange carotenoids is a DNA sequence comprising the aforementioned DNA sequences ① - ⑥. In other words, the gene group used for the synthesis of zeaxanthin-diglucoside is formed by adding the DNA sequence ② to a DNA sequence used for the synthesis of zeaxanthin comprising the DNA sequences ①, ③, ④, ⑤ and ⑥. The gene group includes the one in which the respective DNA sequences constructing the gene group are present on one DNA strand or on different DNA strands individually, or the one which is constructed by the combination of the aforementioned ones according to necessities.

In the case that a plurality of DNA sequences are present on one DNA strand, the arrangement order and direction of the aforementioned DNA sequences ① - ⑥ may be optional provided that the genetic information is capable of expression, that is to say respective genes in a host are in a state of being transcribed and translated appropriately.

One of the typical existing forms of the gene group and the individual DNA sequences is the same as defined in (1).

The biosynthetic pathway of zeaxanthin-diglucoside in *E. coli* is explained as follows: geranylgeranyl pyrophosphate which is a substrate originally present in *E. coli* is converted into prephytoene pyrophosphate by the enzyme encoded by the DNA sequence ⑤, the prephytoene pyrophosphate is converted into phytoene by the enzyme encoded by the DNA sequence ①, the phytoene is then converted into lycopene by the enzyme encoded by the DNA sequence ④, and the lycopene is further converted into β -carotene by the enzyme encoded by the DNA sequence ③, the β -carotene is then converted into zeaxanthin by the enzyme encoded by the DNA sequence ⑥, and the zeaxanthin is finally converted into zeaxanthin-diglucoside by the enzyme encoded by the DNA sequence ② (see Fig. 8).

Zeaxanthin-diglucoside is a carotenoid glycoside having a high water solubility and a pigment which is soluble sufficiently in water at room temperature and exhibits clear yellow. Carotenoid pigments are generally hydrophobic and thus limited on their use as natural coloring materials in foods or the like. Therefore, zeaxanthin-diglucoside settles this defect. Zeaxanthin-diglucoside is isolated from edible plant saffron, *Crocus sativus* (Pure & Appl. Chem., 47, 121-128 (1976)), so that it is thought that its safety for food has been confirmed. Therefore, zeaxanthin-diglucoside is desirable as a yellow natural coloring material of foods or the like. In this connection, there has been heretofore no reports with reference to the isolation of zeaxanthin-diglucoside from microorganisms.

If carotenoid pigments such as lycopene, β -carotene, zeaxanthin and zeaxanthin-diglucoside are intended to be produced, the aforementioned DNA sequences ①, ④ and ⑤, the DNA sequences ①, ③, ④ and ⑤, the DNA sequences ①, ③, ④, ⑤ and ⑥, and the DNA sequences ① - ⑥ are required, respectively, on using *E. coli* as the host. However, when a host other than *E. coli*, particularly the one which is capable of producing carotenoids is used, it has a high possibility of containing also carotenoid precursors at further downstream in the biosynthesis, so that all of the aforementioned DNA sequences ①, ④ and ⑤ (for the production of lycopene), all of the DNA sequences ①, ③, ④ and ⑤ (for the production of β -carotene), all of the DNA sequences ①, ③, ④, ⑤ and ⑥ (for the production of zeaxanthin), or all of the DNA sequences ① - ⑥ (for the production of zeaxanthin-diglucoside) are not always required.

That is to say, only the DNA sequence(s) participating in the formation of an aimed carotenoid pigment from a carotenoid precursor present at the furthest downstream in the host may also be used in this case. Thus, when lycopene is intended to be produced as an aimed carotenoid in a host in which phytoene is preliminarily present, it is also possible to use only the DNA sequence ④ among the DNA sequences ①, ④ and ⑤.

It is also possible to make a host to produce, as the aimed carotenoid pigment relating compound, prephytoene pyrophosphate from geranylgeranyl pyrophosphate by using only the DNA sequence ⑤ of the present invention, or phytoene by using the DNA sequences ① and ⑤ of the present invention or, if the host contains prephytoene pyrophosphate, by using only the DNA sequence ①.

Acquirement of DNA sequences

A method for acquiring the DNA sequences ① - ⑥ which contain the nucleotide sequences coding for the amino acid sequences of the respective enzymes is the chemical synthesis of at least a part of their strand by the method of polynucleotide synthesis. However, if it is taken into consideration that a number of amino acids are bonded, it would be more preferable than the chemical synthesis to acquire the DNA sequences from the DNA library of *Erwinia uredovora* 20D3 ATTC 19321 according to a conventional method in the field of genetic engineering, for example, the hybridization method with a suitable probe.

The individual DNA sequences or the DNA sequence comprising all of these sequences are thus obtained.

Transformant

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The aforementioned gene group comprising a plurality of the DNA sequences ① - ⑥ can be constituted by using the DNA sequences obtained as described above. The DNA sequence thus obtained contains genetic informations for making an enzyme participating in the formation of carotenoids, so that it can be introduced into an appropriate host by the biotechnological method to form a transformant and to produce an enzyme and in its turn a carotenoid pigment or a carotenoid pigment relating compound.

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(1) Host

Plants and a variety of microorganisms, as far as a suitable host-vector system is present, can be the target of transformation by a vector comprising the aforementioned DNA sequences. However, the host is required to contain geranylgeranyl pyrophosphate which is a substrate compound of an enzyme for starting the carotenoid synthesis with use of the DNA sequences of the present invention, or a compound further downstream from it.

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It is known that geranylgeranyl pyrophosphate is synthesized by dimethylallyltransferase which is a common enzyme at the initial stage of the biosynthesis of not only carotenoids but also sterols or terpenes [J. Biochem., 72, 1101-1108 (1972)]. Accordingly, if a cell which cannot synthesize carotenoids can synthesize sterols or terpenes, it probably contains geranylgeranyl pyrophosphate. It is believed that a cell contains at least one of sterols or terpenes.

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Therefore, it is believed theoretically that almost all hosts are capable of synthesizing carotenoids by using the DNA sequences of the present invention as far as a suitable host-vector system is present.

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As the hosts in which the host-vector system is present, there are mentioned plants such as Nicotiana tabacum, Petunia hybrida and the like, microorganism such as bacteria, for example Escherichia coli, Zymomonas mobilis and the like, and yeasts, for example Saccharomyces cerevisiae and the like.

30 (2) Transformation

It is confirmed for the first time by the present invention that the genetic informations present on the DNA sequences of the present invention has been expressed in microorganisms. However, the procedures or the methods for making the transformants (and the production of enzymes or in its turn carotenoid pigments or carotenoid pigment relating compounds by the transformants) are per se conventional in the fields of molecular biology, cell biology or genetic manipulation, and thus the procedures other than described below may be performed in accordance with these conventional techniques.

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In order to express the gene of the DNA sequences according to the present invention in a host, it is necessary to insert the gene into a vector for introducing it into the host. As the vector used in this stage, there is used all of various known vectors such as pBI121 or the like for plants (Nicotiana tabacum, Petunia hybrida); pUC19, pACYC184 or the like for E. coli; pZA22 or the like for Zymomonas mobilis (see Japanese Patent Laid-Open Publication No. 228278/87); and YEpl3 or the like for yeast.

40

On the other hand, it is necessary to transcribe the DNA sequence of the present invention onto mRNA in order to express the gene of the DNA sequence in the host. For this purpose, a promoter as a signal for the transcription may be integrated into the 5'-upstream region from the DNA sequence of the present invention. A variety of promoters such as CaMV35S, NOS, TR1', TR2' (for plants); lac, Tc', CAT, trp (for E. coli); Tc', CAT (for Zymomonas mobilis); ADH1, GAL7, PGK, TRP1 (for yeast) and the like are known as for the promoters, and either of these promoters can be used in the present invention.

45

In the case of procaryote, it is necessary to place ribosome-binding site (SD sequence in E. coli) several base-upstream from the initiation codon (ATG).

50

In this connection, while the aforementioned manipulation is necessary for producing the enzyme protein, one or more of amino acids may be inserted into or added to the polypeptide which is illustrated in the specific ranges of Figs. 1 - 6 (e.g. the polypeptide A - B illustrated in Fig. 1), one or more of amino acids may be deleted, or replaced, as described above.

55

The transformation of the host with the plasmid thus obtained can be conducted optionally by an appropriate method which is conventionally used in the fields of genetic manipulation or cell biology. As for the general matters, there can be referred to appropriate publications or reviews; for example as for the transformation of microorganisms, T. Maniatis, E. F. Fritsch and J. Sambrook: "Molecular Cloning A

Laboratory Manual", Cold Spring Harbor Laboratory (1982).

The transformant is the same as the host used, in its genotype, phenotype or bacteriological properties but for the new trait derived from the genetic information introduced by the DNA sequence of the present invention (that is, the production of an enzyme participating in the carotenoid formation and the synthesis of carotenoids or the like by the enzyme), the trait derived from the vector used and the deletion of the trait corresponding to the deletion of a part of the genetic information of the vector which might be caused on the recombination of genes. *Escherichia coli* JM109 (pCAR1) which is an example of the transformant according to the present invention is deposited as FERM BP-2377.

10 Expression of genetic information/production of carotenoids

The clone of the transformant obtained as described above produces mainly in the transformant an enzyme participating in the carotenoid formation, and a variety of carotenoids or carotenoid pigment relating compounds are synthesized by the enzyme.

15 Culture or the culturing condition of the transformant is essentially the same as those for the host used. Carotenoids can be recovered by the methods, for example, illustrated in Experimental Examples 3 and 4 below.

Furthermore, each enzyme protein coded by each DNA sequence of the present invention is produced mainly in the cell in the case of the transformation of *E. coli*, and it can be recovered by an appropriate method.

BRIEF DESCRIPTION OF THE DRAWINGS

25 Figs. 1 - 6 illustrate the nucleotide sequences in the DNA sequences ① - ⑥ in coding regions, and the amino acid sequences of proteins to be encoded, respectively.

Fig. 7 illustrates the KpnI-HindIII fragment which was acquired from *Erwinia uredovora* 20D3 ATCC 19321 and relates to the biosynthesis of carotenoids, that is the complete nucleotide sequence of the 6918 bp DNA sequence containing the DNA sequences in Figs. 1 - 6, and

Fig. 8 illustrates the function of the polypeptides encoded by the aforementioned DNA sequences ① - ⑥

Experiments

35 All of strains used in the following experiments are deposited in ATCC or other deposition organizations and are freely available.

Experimental Example 1: Cloning of a gene cluster participating in the biosynthesis of a yellow pigment (referred to hereinafter as yellow pigment-synthesizing gene cluster)

40 (1) Preparation of total DNA

Total DNA was prepared from the cells of *Erwinia uredovora* 20D3 ATCC 19321 which had been proliferated until the early-stationary phase in 100 ml of LB medium (1% tryptone, 0.5% yeast extract, 1% NaCl). Penicillin G (manufactured by Meiji Seika) was added to the culture medium so that it has a concentration of 50 units/ml in the medium before 1 hour of the harvest of the cells. After harvesting the cells by centrifugation, this was washed with the TES buffer (20 mM tris, 10 mM EDTA, 0.1 M NaCl, pH 8), heat treated at 68°C for 15 minutes and suspended in Solution I (50 mM glucose, 25 mM Tris, 10 mM EDTA, pH 8) containing 5 mg/ml of lysozyme (manufactured by Seikagaku Kogyo) and 100 µg/ml of RNase A (manufactured by Sigma). The suspension was incubated at 37°C for a period of 30 minutes - 1 hour, and pronase E (manufactured by Kaken Seiyaku) was added so that it had a concentration of 250 µg/ml before incubation at 37°C for 10 minutes. Sodium N-lauroylsarcosine (manufactured by Nacalai tesque) was added so as it had the final concentration of 1%, and the mixture was agitated before incubation at 37°C for several hours. Extraction was conducted several times with phenol/chloroform. While ethanol in volume of 2 equivalents was slowly added, the resulting total DNA was wound around a glass stick, rinsed with 70% ethanol and dissolved in 2 ml of TE buffer (10 mM Tris, 1 mM EDTA, pH 8) to give the total DNA preparation.

(2) Construction of an Escherichia coli cosmid library and acquirement of E. coli transformants producing yellow pigments

Incubation was conducted with 1 unit of restriction enzyme Sau3AI per 50 µl of the total DNA preparation at 37°C for 30 minutes before the inactivation treatment of the restriction enzyme at 68°C for 10 minutes. Many fragments partially digested with Sau3AI were obtained in the neighbourhood of 40 kb under this condition. After the ethanol precipitation of this reaction solution, this half portion was mixed with 2.5 µg of cosmid pJB8 which had been digested with BamHI and treated with alkaline phosphatase and 0.2 µg of a pJB8 Sall-BamHI right arm fragment (smaller fragment) which had been recovered from a gel, and 40 µl of the total amount was subjected to ligation reaction with T4 DNA ligase at 12°C for 2 days. In this connection, the cosmid pJB8 had been previously purchased from Amersham. Restriction enzymes and enzymes used for genetic manipulation were purchased from Boehringer-Mannheim, Takara Shuzo or Wako Pure Chemical Industries. This DNA in which the ligation reaction had been thus performed was used for in vitro packaging with a Gigapack Gold (manufactured by Stratagene, marketed from Funakoshi) to give a large amount of phage particles sufficient for construction of a cosmid library. The phage particles were infected with Escherichia coli DH1 (ATCC 33849). After the cells of E. coli DH1 infected were diluted so as to be 100 colonies per plate, they were plated on a LB plate, cultured at 37°C overnight and further at 30°C for 6 hours or more. As a result, E. coli transformants producing yellow pigments appeared in a proportion of one colony per about 1,100 colonies. These E. coli transformants producing yellow pigments contained plasmids in which 33 - 47 kb Sau3AI partial digestion fragments were inserted into the pJB8.

(3) Location of a yellow pigment-synthesizing gene cluster

A yellow pigment-synthesizing gene cluster was inserted into the pJB8 as the 33 - 47 kb Sau3AI partial digestion fragments. One of these fragments was further subjected to partial digestion with Sau3AI, ligated to the BamHI site of the E. coli vector pUC19 (purchased from Takara Shuzo), and used to transform Escherichia coli JM109 (manufactured by Takara Shuzo). To locate the yellow pigment-synthesizing gene cluster, plasmid DNA's were prepared from 50 E. coli transformants producing yellow pigments which appeared in the LB plate containing ampicillin, and analyzed by agarose gel electrophoresis. As a result, it was found that the smallest inserted fragment was of 8.2 kb. The plasmid containing this 8.2 kb fragment was named as pCAR1 and E. coli JM109 harboring this plasmid was named as Escherichia coli JM109 (pCAR1). This strain produced the same yellow pigments as those of E. urelovora. The 8.2 kb fragment contained a KpnI site in the neighbourhood of the terminal at the lac promoter side and a HindIII site in the neighbourhood at the opposite side. After the 8.2 kb fragment was subjected to double digestion with KpnI/HindIII (HindIII was partially digested; the 8.2 kb fragment had two HindIII sites), the KpnI-HindIII fragment (6.9 kb) was recovered from a gel and ligated to the KpnI-HindIII site of pUC18 (this hybrid plasmid was named as pCAR15). Upon the transformation of E. coli JM109, the E. coli transformant exhibited yellow and produced the same yellow pigments as those of E. urelovora. Accordingly, it was found out that the genes required for the yellow pigment production was located on the KpnI-HindIII fragment (6.9 kb). That is to say, the fragment carrying the yellow pigment-synthesizing genes was capable of being reduced to a 6.9 kb in size.

Experimental Example 2: Analysis of the yellow pigment-synthesizing gene cluster

(1) Determination of the nucleotide sequence of the yellow pigment-synthesizing gene cluster

The complete nucleotide sequence of the 6.9 kb KpnI-HindIII fragment was determined by the kilo-sequence method using Deletion kit for kilo-sequence (manufactured by Takara Shuzo) and the dideoxy method according to Proc. Natl. Acad. Sci. USA, 74 5463-5467 (1977). As a result, it was found that the KpnI-HindIII fragment containing the yellow pigment-synthesizing genes (DNA strand) was 6918 base pairs (bp) in length and its GC content was 54%. The complete nucleotide sequence was shown in Fig. 7 (a) - (g). The KpnI site is represented by the base number 1.

(2) Elucidation of yellow pigment-synthesizing gene cluster

The HindIII side of the 6918 bp fragment (DNA strand) containing the yellow pigment-synthesizing genes (right terminal side in Fig. 7) was deleted with Deletion kit for kilo-sequence. A hybrid plasmid (designated pCAR25) was constructed by inserting a 1 - 6503 fragment, which was obtained by deletion

from the *Hind*III site to nucleotide position 6504, into pUC19. *E. coli* JM109 harboring pCAR25 [referred to hereinafter as *E. coli* (pCAR25)] exhibited yellow and produced the same yellow pigments as those of *E. uredovora*. Therefore, it was thought that the region from the base number 6504 to 6918 in Fig. 7 was not required for yellow pigment production. The nucleotide sequence in the region from the base number 1 to 6503 in the 6918 bp DNA sequence containing the yellow pigment-synthesizing genes was analyzed. As a result, it was found that there were six open reading frames (ORFs). That is to say, there were an ORF coding for a polypeptide with a molecular weight of 32,583 from the base number 225 to 1130 (referred to as ORF1, which corresponds to A - B in Figs. 1 and 7), an ORF coding for a polypeptide with a molecular weight of 47,241 from the base number 1143 - 2435 (referred to as ORF2, which corresponds to C - D in Figs. 2 and 7), an ORF coding for a polypeptide with a molecular weight of 43,047 from the base number 2422 to 3567 (referred to as ORF3, which corresponds to E - F in Figs. 3 and 7), an ORF coding for a polypeptide with a molecular weight of 55,007 from the base number 3582 to 5057 (referred to as ORF4, which corresponds to G - H in Figs. 4 and 7), an ORF coding for a polypeptide with a molecular weight of 33,050 from the base number 5096 to 5983 (referred to as ORF5, which corresponds to I - J in Figs. 5 and 7), and an ORF coding for a polypeptide with a molecular weight of 19,816 from the base number 6452 to 5928 (referred to as ORF6, which corresponds to K - L in Figs. 6 and 7. Only this ORF6 has the opposite orientation with the others). In this connection, each ORF contained at positions several base-upstream from its initiation codon the SD (Shine-Dalgarno) sequence which is homologous with the 3'-region of 16S ribosomal RNA of *E. coli*. Thus, it was thought that polypeptides were in fact synthesized in *E. coli* by these six ORFs. This was confirmed by the following *in vitro* transcription-translation experiment.

That is to say, the *in vitro* transcription-translation analysis was carried out with DNA in which the plasmid pCAR25 containing ORF1 - ORF6 had been digested with *Sal*I and with DNAs in which respective fragments containing respective ORFs (containing the SD sequence) of ORF1 - ORF6 had been digested with appropriate restriction enzymes, isolated, inserted into pUC19 or pUC18 so that it was subjected to transcriptional read-through from a *lac* promoter, and then digested with *Sal*I. In this experiment, a Prokaryotic DNA-directed translation kit manufactured by Amersham was used. As a result, it was confirmed that the bands of polypeptides corresponding to the aforementioned respective ORFs were detected as the transcription-translation products.

Moreover, all of six ORFs were necessary for production of the same yellow pigments as those of *E. uredovora* as described below (Experimental Examples 3, 4 and 5). From these results, ORF1, ORF2, ORF3, ORF4, ORF5 and ORF6 were designated as *crtE*, *crtX*, *crtY*, *crtI*, *crtB* and *crtZ* genes, respectively.

The base numbers in Figs. 1 - 6 were represented on the basis of the *Kpn*I site in Fig. 7 as the base number 1 and correspond to each other. The marks A - L in Figs. 1 - 6 correspond to the marks A - L in Fig. 7. The DNA sequence from K to L in Fig. 6 was that of the complementary strand of the DNA sequence from K to L in Fig. 7. That is to say, the DNA sequence illustrated in Fig. 6 has the opposite orientation in transcription with the DNA sequences in Figs. 1 - 5 in the original DNA sequence (Fig. 7).

(3) Analysis of homology by the DNA-DNA hybridization method

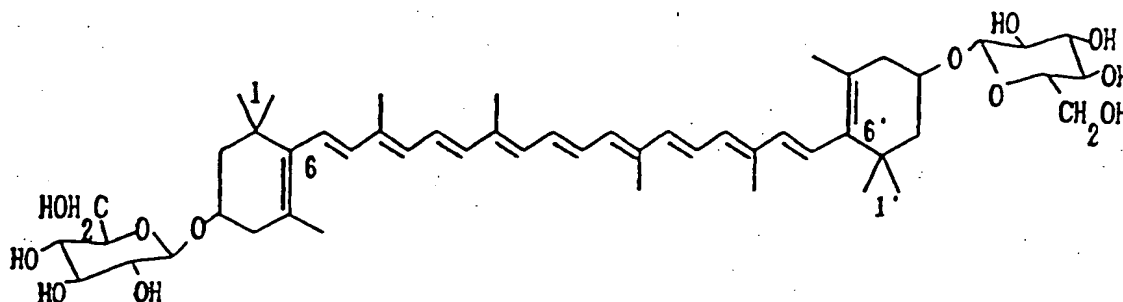
Total DNA of *Erwinia herbicola* Eho 10 ATCC 39368 was prepared in the same manner as in Experimental Example 1 (1). A 7.6 kb fragment containing the DNA sequence in Fig. 7 was cut out from the hybrid plasmid pCAR1 by *Kpn*I digestion and labeled with DNA labeling & detection kit nonradioactive (manufactured by Boehringer-Mannheim) according to the DIG-ELISA method to give probe DNA. The homology of total DNAs (intact or *Kpn*I digested) of *E. herbicola* Eho 10 ATCC 39368 and *E. uredovora* 20D3 ATCC 19321 with this probe DNA was analyzed by the DNA-DNA hybridization method with the aforementioned DNA labeling & detection kit nonradioactive. As a result, the probe DNA was hybridized strongly with total DNA of the latter *E. uredovora* 20D3 ATCC 19321, but not at all with total DNA of the former *E. herbicola* Eho 10 ATCC 39368. Also, the restriction map deduced from the DNA sequence in Fig. 7 was quite different from that reported in J. Bacteriol., 168, 607-612 (1986). It was concluded from the above described results that the DNA sequence in Fig. 7, that is, the DNA sequences useful for the synthesis of carotenoids according to the present invention exhibits no homology with the DNA sequence containing the yellow pigment-synthesizing genes of *E. herbicola* Eho 10 ATCC 39368.

Experimental Example 3: Analysis of yellow pigments

E. coli (pCAR25) produced the same yellow pigments as those of *E. uredovora* 20D3 ATCC 19321 and *E. herbicola* Eho 10 ATCC 39368, and its yield was 5 times higher than those of the former and 6 times higher than those of the latter (per dry weight). The cells harvested from 8 liters of 2 × YT medium (1.6%

tryptone, 1% yeast extract, 0.5% NaCl) were extracted once with 1.2 liter of methanol. The methanol extract was evaporated to dryness, dissolved in methanol, and subjected to thin layer chromatography (TLC) with silica gel 60 (Merck) (developed with chloroform : methanol = 4:1). The yellow pigments were separated into 3 spots having R_f values of 0.93, 0.62 and 0.30 by TLC. The yellow (to orange) pigment at the R_f value of 0.30 which was the strongest spot was scraped up from the TLC plate, extracted with a small amount of methanol, loaded on a Sephadex LH-20 column for chromatography [30 cm x 3.0 cm (Ø)] and developed and eluted with methanol to give 4 mg of a pure product. The yellow (to orange) pigment obtained was sparingly soluble in organic solvents other than methanol and easily soluble in water, so that it was suggested that it might be a carotenoid glycoside. Such suggestion was also supported from a molecular weight of 892 by FD-MS spectrum (the mass of this pigment was larger than that of zeaxanthin (described hereinafter) by the mass of two glucose). When this substance was hydrolyzed with 1N HCl at 100 °C for 10 minutes, zeaxanthin was obtained. Then, acetylation was conducted according to the usual method. That is, the substance was dissolved in 10 ml of pyridine, large excess of acetic anhydride was added, and the mixture was stirred at room temperature and left standing overnight. After the completion of reaction, water was added to the mixture and chloroform extraction was carried out. The chloroform extract was concentrated and loaded on a silica gel column [30 cm x 3.0 cm (Ø)] for chromatography to develop and elute with chloroform. Measurement of ¹H-NMR gave the spectrum identical with the tetraacetyl derivative of zeaxanthin-β-diglucoside [Helvetica Chimica Acta, 57, 1641-1651 (1974)], so that the substance was identified as zeaxanthin-β-diglucoside (its structure being illustrated below).

The yield was 1.1 mg/g dry weight. The substance had a solubility of at least 2 mg in 100 ml of water and methanol, and water was superior to methanol in solubility of the substance. The substance had low solubilities in chloroform and acetone, and its solubilities were 0.5 mg in 100 ml of these solvents.



Experimental Example 4: Analysis of the metabolic intermediates of carotenoids

(1) Construction of various deletion plasmids

A hybrid plasmid (designated as pCAR16) was constructed by inserting a 1-6009 fragment, which was obtained by deletion to nucleotide position 6010 from the HindIII site (right terminal in Fig. 7) of the 6918 bp fragment containing the yellow pigment-synthesizing genes (DNA strand) (Fig. 7) using Deletion kit for kilobase. pCAR16 contains the genes from crtE, crtX, crtY, crtI, crtB and crtZ. Various deletion plasmids were constructed, as shown in Table 1, on the basis of the pCAR16 and the aforementioned hybrid plasmid pCAR25 (containing genes crtE, crtX, crtY, crtI, crtB and crtZ).

Table 1: Construction of various deletion plasmids

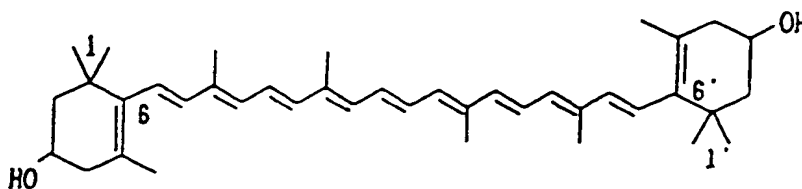
The number within parentheses behind the name of respective restriction enzymes represents the number of base at the initial recognition site of the restriction enzyme. The base numbers correspond to those in Figs. 1 - 6 and Fig. 7. Analysis of the metabolic intermediates of carotenoids was performed using the transformants of E. coli JM109 by various deletion plasmids [referred to hereinafter as E. coli (name of plasmid)].

Table 1

Plasmid	Construction method	Genes functioning
pCAR25	See text	<u>crtE crtX crtY crtI crtB crtZ</u>
pCAR25delB	Frame shift in <u>BstEII</u> (1235) of pCAR25	<u>crtE crtY crtI crtB crtZ</u>
pCAR16	See text	<u>crtE crtX crtY crtI crtB</u>
pCAR16delB	Frame shift in <u>BstEII</u> (1235) of pCAR16	<u>crtE crtY crtI crtB</u>
pCAR16delC	Frame shift in <u>SnaBI</u> (3497) of pCAR16	<u>crtE crtX crtI crtB</u>
pCAR-ADE	Deletion of the <u>BstEII</u> (1235) - <u>SnaBI</u> (3497) fragment from pCAR16	<u>crtE crtI crtB</u>
pCAR-ADEF	Deletion of the <u>BstEII</u> (1235) - <u>SnaBI</u> (3497) fragment from pCAR25	<u>crtE crtI crtB crtZ</u>
pCAR25delD	Frame shift in <u>BamHI</u> (3652) of pCAR25	<u>crtE crtX crtY crtB crtZ</u>
pCAR-AE	Deletion of the <u>BstEII</u> (1235) - <u>BamHI</u> (3652) fragment from pCAR16	<u>crtE crtB</u>
pCAR-A	Insertion of the <u>KpnI</u> (1) - <u>BstEII</u> (1235) fragment in pUC19	<u>crtE</u>
pCAR-E	Insertion of the <u>Eco52I</u> (4926) - 6009 fragment in pUC19	<u>crtB</u>
pCAR25delE	Frame shift in <u>MluI</u> (5379) of pCAR25	<u>crtE crtX crtY crtI crtZ</u>
pCAR25delA	Frame shift in <u>AvaI</u> (995) of pCAR25	<u>crtX crtY crtI crtB crtZ</u>
pCAR-CDE	Insertion of the <u>Sall</u> (2295) - 6009 fragment in pUC19	<u>crtY crtI crtB</u>

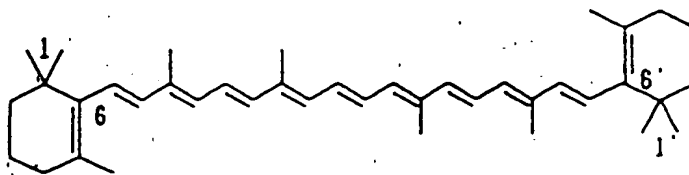
(2) Identification of zeaxanthin

The cells harvested from 3 liters of 2 × YT medium of *E. coli* (pCAR25delB) (exhibiting orange) were extracted twice with 400 ml portions of acetone at low temperature, concentrated, then extracted with chloroform:methanol (9:1) and evaporated to dryness. This was subjected to silica gel column chromatography [30 cm × 3.0 cm (Ø)]. After the column was washed with chloroform, an orange band was eluted with chloroform:methanol (100:1). This pigment was dissolved in ethanol, recrystallized at low temperature to give 8 mg of a pure product. The analysis by its UV-visible absorption, ¹H-NMR, ¹³C-NMR and FD-MS (m/e 568) spectra revealed that this substance had the same structure except for stereochemistry as zeaxanthin (β,β-carotene-3,3'-diol). It was then dissolved in diethyl ether : isopentane : ethanol (5:5:2), and the CD spectrum was measured. As a result, it was found that this substance had a 3R,3'R-stereochemistry [Phytochemistry, 27, 3605-3609 (1988)]. Therefore, it was identified as zeaxanthin (β,β-carotene-3R,3'R-diol), of which the structure is illustrated below. The yield was 2.2 mg/g dry weight. This substance corresponded to the yellow pigment having an R_f value of 0.93 in Experimental Example (1).



(3) Identification of β -carotene

The cells harvested from 3 liters of LB medium of *E. coli* (pCAR16) (exhibiting orange) were extracted 3 times with 500 ml portions of cold methanol at low temperature and the methanol extract was further extracted with 1.5 liter of hexane. The hexane layer was concentrated and subjected to silica gel column chromatography [30 cm \times 3.0 cm (\varnothing)]. Development and elution were conducted with hexane:ethyl acetate (50:1) to collect an orange band. The orange fraction was concentrated and recrystallized from ethanol to give 8 mg (reduced weight without moisture). This substance was presumed to belong to β -carotene from its UV-visible absorption spectrum, and a molecular weight of 536 by FD-MS spectrum also supported this presumption. Upon comparing this substance with the authentic sample (Sigma) of β -carotene by ^{13}C -NMR spectrum, all of chemical shifts of carbons were identical with each other. Thus, this substance was identified as β -carotene (all-trans- β , β -carotene, of which the structure was illustrated below). It was also confirmed by the similar method that *E. coli* (pCAR16delB) accumulated the same β -carotene as described above. Its yield was 2.0 mg/g dry weight, which corresponded to 2 - 8 times (per dry weight) of the total carotenoid yield in carrot (Kintokininjin) culture cells described in Soshikibaiyou (The Tissue Culture), 13, 379-382 (1987).



(4) Identification of lycopene

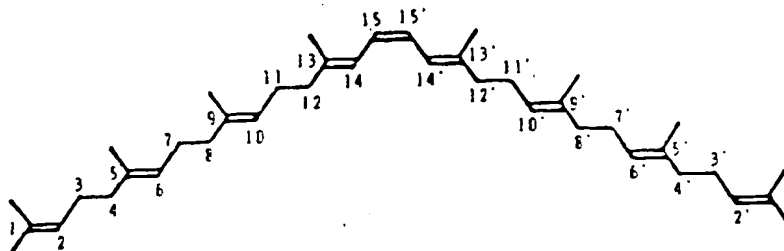
The cells harvested from 3 liters of LB medium of *E. coli* (pCAR16delC) (exhibiting red) were extracted once with 500 ml of cold methanol at low temperature, and the precipitate by centrifugation was extracted again with 1.5 liter of chloroform. The chloroform layer was concentrated and subjected to silica gel chromatography [30 cm \times 3.0 cm (\varnothing)]. Development and elution were conducted with hexane:chloroform (1:1) to collect a red band. This fraction was concentrated. This substance was presumed to belong to lycopene from its UV-visible absorption spectrum, and a molecular weight of 536 by FD-MS spectrum also supported this presumption. Upon comparing this substance with the authentic sample (Sigma) of lycopene by ^1H -NMR spectrum, all of chemical shifts of hydrogens were identical with each other. When, this substance and the authentic sample were subjected to TLC with silica gel 60 (Merck) [developed with hexane:chloroform (50:1)] and with RP-18 [developed with methanol:chloroform (4:1)], the displacement distances of these samples were completely equal to each other. Thus this substance was identified as lycopene (all-trans- β , β -carotene, of which the structure was illustrated below). It was also confirmed by the similar method that *E. coli* (pCAR-ADE) and *E. coli* (pCAR-ADEF) accumulated the same lycopene as described above. The yield of the former was 2.0 mg/g dry weight, which corresponded to 2 times (per dry weight) of the total carotenoid yield in a hyperproduction derivative of carrot (Kintokininjin) culture cells described in Soshikibaiyou (The Tissue Culture), 13, 379-382 (1987).



(5) Identification of phytoene

The cells harvested from 1.5 liter of 2 \times YT medium of *E. coli* (pCAR-AE) were extracted twice with 200 ml portions of acetone and twice with 100 ml portions of hexane, and evaporated to dryness. This was subjected to silica gel chromatography [30 cm \times 3.0 cm (\varnothing)]. Development and elution were conducted

with hexane:chloroform (1:1) to collect a band which had a strong UV absorption, and it was confirmed to be phytoene by its UV absorption spectrum. It was further subjected to LH-20 column chromatography [30 cm x 3.0 cm (Ø)]. Development and elution were conducted with chloroform:methanol (1:1) to give 4 mg of a pure product. The comparison of the ¹H-NMR spectrum of this substance with the ¹H-NMR spectra of *trans*- and *cis*-phytoen (J. Magnetic Resonance, 10, 43-50 (1973)) showed this substance to be a mixture of the *trans*- and *cis*-isomers. Isomerization from *trans*-isomer to *cis*-isomer hardly occurs, and thus it was judged that such a mixture was produced as a result of *cis-trans* isomerization in the course of the purification. Therefore, it was concluded that the original phytoene was the *cis*-type phytoene (15,15'-*cis*-phytoene, of which the structure is shown below). It was also confirmed by the similar method that *E. coli* (pCAR25delD) accumulated the same phytoene as described above.



Experimental Example 5: Identification of carotenoid biosynthesis genes

From the facts that *E. coli* (pCAR25) produced zeaxanthin-diglucoside and that *E. coli* (pCAR25delB) harboring a plasmid, in which *crtX* had been removed from pCAR25, accumulated zeaxanthin, it was found that the *crtX* gene encoded the glycosylation enzyme which was capable of converting zeaxanthin into zeaxanthin-diglucoside. Similarly, from the fact that *E. coli* (pCAR16delB) harboring a plasmid, in which *crtZ* had been removed from pCAR25delB, accumulated β -carotene, it was found that the *crtZ* gene encoded the hydroxylation enzyme which was capable of converting β -carotene into zeaxanthin. Similarly, from the fact that the *E. coli* (pCAR-ADE) harboring a plasmid, in which *crtY* had been removed from pCAR16delB, accumulated lycopene, it was found that the *crtY* gene encoded the cyclization enzyme which was capable of converting lycopene into β -carotene. Also, *E. coli* (pCAR-ADEF) carrying both of the *crtE*, *crtI* and *crtB* genes required for producing lycopene and the *crtZ* gene encoding the hydroxylation enzyme was able to synthesize only lycopene. This demonstrates directly that the hydroxylation reaction in carotenoid biosynthesis occurs after the cyclization reaction. Further, from the facts that *E. coli* (pCAR-ADE) accumulated lycopene and that *E. coli* (pCAR-AE) harboring a plasmid, in which the *crtI* gene had been removed from pCAR-ADE, accumulated phytoene, it was found that the *crtI* gene encoded the desaturation enzyme which was capable of converting phytoene into lycopene. *E. coli* (pCAR-A) and *E. coli* (pCAR-E) were not able to produce phytoene. It was thought from this result that both of the *crtE* and *crtB* genes were required for producing phytoene in *E. coli*. *crtB* and *crtE* were identified as the gene for the conversion of geranylgeranyl pyrophosphate into prephytoene pyrophosphate and that for the conversion of prephytoene pyrophosphate into phytoene, by comparing their putative amino acid sequence with those of *crtB* and *crtE* gene products in a photo synthetic bacterium *Rhodobacter capsulatus* [Mol. Gen. Genet., 216, 254-268 (1988)]. From these analyses described above, all of the six *crt* genes have been identified and the biosynthetic pathway of carotenoids have also been clear. These results are listed in Fig. 8.

E. coli (pCAR25delE) accumulated no detectable carotenoid intermediate, while *E. coli* (pCAR25delA) and *E. coli* (pCAR-CDE) were able to produce a small amount of carotenoids. That is to say, *E. coli* (pCAR25delA) and *E. coli* (pCAR-CDE) produced 4% of zeaxanthin-diglucoside and 2% of β -carotene as compared with the *E. coli* (pCAR25) and the *E. coli* (pCAR16delB), respectively. This result suggests that the reaction from prephytoene pyrophosphate to phytoene may occur non-enzymatically notwithstanding the yield being trace.

As described above, the detailed biosynthetic pathway of carotenoids including general and famous carotenoids such as lycopene, β -carotene and zeaxanthin and water soluble carotenoid such as zeaxanthin-diglucoside were for the first time elucidated, and the gene cluster useful for these biosynthesis was capable of being acquired for the first time. In this connection, lycopene, β -carotene and zeaxanthin which were produced by the genes in the aforementioned Experimental Examples were stereochemically identical

with those derived from higher plants [T.W. Goodwin: "Plant Pigments", Academic Press (1988)].

As for zeaxanthin-digluconide, the isolation from a plant was only reported [Pure & Appl. Chem., 47, 121-128 (1976)], but its isolation from microorganisms has not been reported.

5 Experimental Example 6: Synthesis of carotenoids in Zymomonas

Zymomonas mobilis is a facultative anaerobic ethanol-producing bacterium. It has a higher ethanol producing rate than that of yeast (Saccharomyces cerevisiae), so that it is preferable as a fuel alcohol-producing bacterium in future. Also, Zymomonas has a special metabolic pathway, Entner-Doudoroff but not glycolytic pathway and cannot produce carotenoids. In order to add further values to this bacterium, the carotenoid biosynthesis genes were introduced into Zymomonas.

The 7.6 kb fragment containing the DNA sequence shown in Fig. 7 was cut out from the hybrid plasmid pCAR1 by KpnI digestion and treated with DNA polymerase I (Klenow enzyme). The fragment thus treated was ligated to the EcoRV site of the cloning vector pZA22 for Zymomonas [see Agric. Biol. Chem., 50, 3201-3203 (1986) and Japanese Patent Laid-Open Publication No. 228278/87] to construct a hybrid plasmid pZACAR1. Also, the 1 - 6009 fragment in the DNA sequence in Fig. 7 was cut out from pCAR16 by KpnI/EcoRI digestion and treated with DNA polymerase I (Klenow enzyme). The fragment thus treated was ligated to the EcoRV site of pZA22 to construct a hybrid plasmid pZACAR16. The orientation of the inserted fragments in these plasmids were opposite with the orientation of the Tc^r gene on taking the orientation in Fig. 7 as the normal one. These plasmids were introduced into Z. mobilis NRRL B-14023 by conjugal transfer with the helper plasmid pRK2013 (ATCC 37159) and stably maintained in this strain. Z. mobilis NRRL B-14023 in which pZACAR1 and pZACAR16 had been introduced exhibited yellow, and produced zeaxanthin-digluconide in an amount of 0.28 mg/g dry weight and β -carotene in an amount of 0.14 mg/g dry weight, respectively. Therefore, carotenoids were successfully produced in Zymomonas by the carotenoid biosynthesis genes according to the present invention.

Deposition of Microorganism

Microorganism relating to the present invention is deposited at Fermentation Research Institute, Japan as follows:

Microorganism	Accession number	Date of deposit
<u>Escherichia coli</u> JM109 (pCAR1)	FERM BP 2377	April 11, 1989

Claims

1. A DNA sequence selected from the following group and encoding an enzyme polypeptide which participates in carotenoid biosynthesis proceeding via geranylgeranyl pyrophosphate, phytoene and zeaxanthin-digluconide:

a DNA sequence encoding an enzyme polypeptide which participates in a step before the phytoene stage in the carotenoid biosynthesis and whose amino acid sequence corresponds substantially to the amino acid sequence from A to B shown in Figs. 1(a) and (b);

a DNA sequence encoding a polypeptide which has the enzymatic activity of converting zeaxanthin into zeaxanthin-digluconide in the carotenoid biosynthesis and whose amino acid sequence corresponds substantially to the amino acid sequence from C to D shown in Figs. 2(a) and (b);

a DNA sequence encoding a polypeptide which has the enzymatic activity of converting lycopene into β -carotene in the carotenoid biosynthesis and whose amino acid sequence corresponds substantially to the amino acid sequence from E to F shown in Figs. 3(a) and (b);

a DNA sequence encoding a polypeptide which has the enzymatic activity of converting phytoene into lycopene in the carotenoid biosynthesis and whose amino acid sequence corresponds substantially to the amino acid sequence from G to H shown in Figs. 4(a),(b) and (c);

a DNA sequence encoding a polypeptide which has the enzymatic activity of converting geranylgeranyl pyrophosphate as a substrate into a next carotenoid compound in the carotenoid biosynthesis and whose amino acid sequence corresponds substantially to the amino acid sequence from I to J shown in Figs. 5(a) and (b); and

a DNA sequence encoding a polypeptide which has the enzymatic activity of converting β -carotene

into zeaxanthin in the carotenoid biosynthesis and whose amino acid sequence corresponds substantially to the amino acid sequence from K to L shown in Figs. 6.

2. A DNA sequence according to claim 1, which encodes an enzyme polypeptide participating in a step before the phytoene stage in the carotenoid biosynthesis and having the amino acid sequence corresponding substantially to the amino acid sequence from A to B shown in Figs. 1(a) and (b).
3. A DNA sequence according to claim 1, which encodes a polypeptide having the enzymatic activity of converting zeaxanthin into zeaxanthin-diglucoside in the carotenoid biosynthesis and having the amino acid sequence corresponding substantially to the amino acid sequence from C to D shown in Figs. 2(a) and (b).
4. A DNA sequence according to claim 1, which encodes a polypeptide having the enzymatic activity of converting lycopene into β -carotene in the carotenoid biosynthesis and having the amino acid sequence corresponding substantially to the amino acid sequence from E to F shown in Figs. 3(a) and (b).
5. A DNA sequence according to claim 1, which encodes a polypeptide having the enzymatic activity of converting phytoene into lycopene in the carotenoid biosynthesis and having the amino acid sequence corresponding substantially to the amino acid sequence from G to H shown in Figs. 4(a),(b) and (c).
6. A DNA sequence according to claim 1, which encodes a polypeptide having the enzymatic activity of converting geranylgeranyl pyrophosphate as a substrate into a next carotenoid compound in the carotenoid biosynthesis and having the amino acid sequence corresponding substantially to the amino acid sequence from I to J shown in Figs. 5(a) and (b).
7. A DNA sequence according to claim 1, which encodes a polypeptide having the enzymatic activity of converting β -carotene into zeaxanthin in the carotenoid biosynthesis and having the amino acid sequence corresponding substantially to the amino acid sequence from K to L shown in Figs. 6.
8. Process for producing a carotenoid or a precursor compound which is selected from the group consisting of phytoene, lycopene, β -carotene, zeaxanthin and zeaxanthin-diglucoside, characterised in that a host is transformed with at least one of the DNAs selected from the following DNA sequences encoding the enzyme polypeptides which participate in carotenoid biosynthesis proceeding via geranylgeranyl pyrophosphate, phytoene and zeaxanthin-diglucoside:
 - a DNA sequence encoding an enzyme polypeptide which participates in the step before the phytoene stage in the carotenoid biosynthesis and whose amino acid sequence corresponds substantially to the amino acid sequence from A to B shown in Figs. 1(a) and (b);
 - a DNA sequence encoding a polypeptide which has the enzymatic activity of converting zeaxanthin into zeaxanthin-diglucoside in the carotenoid biosynthesis and whose amino acid sequence corresponds substantially to the amino acid sequence from C to D shown in Figs. 2(a) and (b);
 - a DNA sequence encoding a polypeptide which has the enzymatic activity of converting lycopene into β -carotene in the carotenoid biosynthesis and whose amino acid sequence corresponds substantially to the amino acid sequence from E to F shown in Figs. 3(a) and (b);
 - a DNA sequence encoding a polypeptide which has the enzymatic activity of converting phytoene into lycopene in the carotenoid biosynthesis and whose amino acid sequence corresponds substantially to the amino acid sequence from G to H shown in Figs. 4(a),(b) and (c);
 - a DNA sequence encoding a polypeptide which has the enzymatic activity of converting geranylgeranyl pyrophosphate as a substrate into a next carotenoid compound in the carotenoid biosynthesis and whose amino acid sequence corresponds substantially to the amino acid sequence from I to J shown in Figs. 5(a) and (b); and
 - a DNA sequence encoding a polypeptide which has the enzymatic activity of converting β -carotene into zeaxanthin in the carotenoid biosynthesis and whose amino acid sequence corresponds substantially to the amino acid sequence from K to L shown in Figs. 6;
 and the transformant is cultured.

Patentansprüche

1. DNS-Sequenz, die aus der folgenden Gruppe ausgewählt ist und ein Enzym-Polypeptid codiert, das an der über Geranylgeranylpyrophosphat, Phytoen und Zeaxanthindiglycosid verlaufenden Carotinoid-Biosynthese beteiligt ist:

DNS-Sequenz, die ein Enzym-Polypeptid codiert, das bei der Carotinoid-Biosynthese auf einer Stufe vor der Phytoenstufe beteiligt ist und dessen Aminosäuresequenz im wesentlichen der in Fig. 1(a) und (b) von A bis B dargestellten Aminosäuresequenz entspricht;

DNS-Sequenz, die ein Polypeptid codiert, das die enzymatische Aktivität der Umwandlung von Zeaxanthin in Zeaxanthindiglycosid bei der Carotinoid-Biosynthese besitzt und dessen Aminosäuresequenz im wesentlichen der in FIG.2(a) und (b) von C bis D dargestellten Aminosäuresequenz entspricht;

DNS-Sequenz, die ein Polypeptid codiert, das die enzymatische Aktivität der Umwandlung von Lycopin in β -Carotin bei der Carotinoid-Biosynthese aufweist und dessen Aminosäuresequenz im wesentlichen der in Fig. 3(a) und (b) von E bis F dargestellten Aminosäuresequenz entspricht;

DNS-Sequenz, die ein Polypeptid codiert, das die enzymatische Aktivität der Umwandlung von Phytoen in Lycopin bei der Carotinoid-Biosynthese aufweist und dessen Aminosäuresequenz im wesentlichen der in Fig. 4(a), (b) und (c) von G bis H dargestellten Aminosäuresequenz entspricht;

DNS-Sequenz, die ein Polypeptid codiert, das die enzymatische Aktivität der Umwandlung von Geranylgeranylpyrophosphat bei der Carotinoid-Biosynthese in die nächste Carotinoid-Verbindung aufweist und dessen Aminosäuresequenz im wesentlichen der in Fig. 5(a) und (b) von I bis J dargestellten Aminosäuresequenz entspricht; und

DNS-Sequenz, die ein Polypeptid codiert, das die enzymatische Aktivität der Umwandlung von β -Carotin in Zeaxanthin bei der Carotinoid-Biosynthese aufweist und dessen Aminosäuresequenz im wesentlichen der in Fig. 6 von K bis L dargestellten Aminosäuresequenz entspricht.

2. DNS-Sequenz gemäß Anspruch 1, die ein Enzym-Polypeptid codiert, das in der Carotinoid-Biosynthese auf einer Stufe vor der Phytoenstufe beteiligt ist und eine Aminosäuresequenz aufweist, die im wesentlichen der in Fig. 1(a) und (b) von A bis B dargestellten Aminosäuresequenz entspricht.

3. DNS-Sequenz gemäß Anspruch 1, die ein Polypeptid codiert, das die enzymatische Aktivität der Umwandlung von Zeaxanthin in Zeaxanthindiglycosid bei der Carotinoid-Biosynthese besitzt und eine Aminosäuresequenz aufweist, die im wesentlichen der in Fig. 2(a) und (b) von C bis D dargestellten Aminosäuresequenz entspricht.

4. DNS-Sequenz gemäß Anspruch 1, die ein Polypeptid codiert, das die enzymatische Aktivität der Umwandlung von Lycopin in β -Carotin bei der Carotinoid-Biosynthese besitzt und eine Aminosäuresequenz aufweist, die im wesentlichen der in Fig. 3(a) und (b) von E bis F dargestellten Aminosäuresequenz entspricht.

5. DNS-Sequenz gemäß Anspruch 1, die ein Polypeptid codiert, das die enzymatische Aktivität der Umwandlung von Phytoen in Lycopin bei der Carotinoid-Biosynthese besitzt und eine Aminosäuresequenz aufweist, die im wesentlichen der in Fig. 4(a), (b) und (c) von G bis H dargestellten Aminosäuresequenz entspricht.

6. DNS-Sequenz gemäß Anspruch 1, die ein Polypeptid codiert, das die enzymatische Aktivität der Umwandlung von Geranylgeranylpyrophosphat als Substrat bei der Carotinoid-Biosynthese in die nächste Carotinoidverbindung besitzt und eine Aminosäuresequenz aufweist, die im wesentlichen der in Fig. 5(a) und (b) von I bis J dargestellten Aminosäuresequenz entspricht.

7. DNS-Sequenz gemäß Anspruch 1, die ein Polypeptid codiert, das die enzymatische Aktivität der Umwandlung von β -Carotin in Zeaxanthin bei der Carotinoid-Biosynthese besitzt und eine Aminosäuresequenz aufweist, die im wesentlichen der in Fig. 6 von K bis L dargestellten Aminosäuresequenz entspricht.

8. Verfahren zur Herstellung eines Carotinoids oder einer Vorläuferverbindung aus der Gruppe Phytoen, Lycopin, β -Carotin, Zeaxanthin und Zeaxanthindiglycosid, dadurch gekennzeichnet,

daß ein Wirt mit mindestens einer der aus den folgenden DNS-Sequenzen ausgewählten Desoxyribonucleinsäuren transformiert wird, die die Enzym-Polypeptide codieren, die bei der über Geranylgeranylpyrophosphat, Phytoen und Zeaxanthindiglucoosid verlaufenden Carotinoid-Biosynthese beteiligt sind:

DNS-Sequenz, die ein Enzym-Polypeptid codiert, das bei der Carotinoid-Biosynthese auf einer Stufe vor der Phytoenstufe beteiligt ist und dessen Aminosäuresequenz im wesentlichen der in Fig. 1(a) und (b) von A bis B dargestellten Aminosäuresequenz entspricht;

DNS-Sequenz, die ein Polypeptid codiert, das die enzymatische Aktivität der Umwandlung von Zeaxanthin in Zeaxanthindiglucoosid bei der Carotinoid-Biosynthese besitzt und dessen Aminosäuresequenz im wesentlichen der in FIG.2(a) und (b) von C bis D dargestellten Aminosäuresequenz entspricht;

DNS-Sequenz, die ein Polypeptid codiert, das die enzymatische Aktivität der Umwandlung von Lycopin in β -Carotin bei der Carotinoid-Biosynthese aufweist und dessen Aminosäuresequenz im wesentlichen der in Fig. 3(a) und (b) von E bis F dargestellten Aminosäuresequenz entspricht;

DNS-Sequenz, die ein Polypeptid codiert, das die enzymatische Aktivität der Umwandlung von Phytoen in Lycopin bei der Carotinoid-Biosynthese aufweist und dessen Aminosäuresequenz im wesentlichen der in Fig. 4(a), (b) und (c) von G bis H dargestellten Aminosäuresequenz entspricht;

DNS-Sequenz, die ein Polypeptid codiert, das die enzymatische Aktivität der Umwandlung von Geranylgeranylpyrophosphat bei der Carotinoid-Biosynthese in die nächste Carotinoid-Verbindung aufweist und dessen Aminosäuresequenz im wesentlichen der in Fig. 5(a) und (b) von I bis J dargestellten Aminosäuresequenz entspricht; und

DNS-Sequenz, die ein Polypeptid codiert, das die enzymatische Aktivität der Umwandlung von β -Carotin in Zeaxanthin bei der Carotinoid-Biosynthese aufweist und dessen Aminosäuresequenz im wesentlichen der in Fig. 6 von K bis L dargestellten Aminosäuresequenz entspricht; und das Transformationsprodukt gezüchtet wird.

Revendications

1. Séquence d'ADN choisie parmi l'ensemble ci-après, et codant un polypeptide enzymatique qui participe à la biosynthèse des caroténoïdes par l'intermédiaire du pyrophosphate de géranylgéranyle, du phytoène et du zéaxanthine-diglucooside :

une séquence d'ADN codant un polypeptide enzymatique qui participe à une étape préalable à la phase phytoène de la biosynthèse des caroténoïdes, et dont la séquence d'acides aminés correspond essentiellement à la séquence d'acides aminés allant de A à B sur les figures 1(a) et (b) ;

une séquence d'ADN codant un polypeptide qui a une activité enzymatique de conversion de la zéaxanthine en zéaxanthine-diglucooside dans la biosynthèse des caroténoïdes, et dont la séquence d'acides aminés correspond essentiellement à la séquence d'acides aminés allant de C à D sur les figures 2(a) et (b) ;

une séquence d'ADN codant un polypeptide qui a une activité enzymatique de conversion du lycopène en β -carotène dans la biosynthèse des caroténoïdes et dont la séquence d'acides aminés correspond essentiellement à la séquence d'acides aminés allant de E à F sur les figures 3(a) et (b) ;

une séquence d'ADN codant un polypeptide qui a une activité enzymatique de conversion du phytoène en lycopène dans la biosynthèse des caroténoïdes, et dont la séquence d'acides aminés correspond essentiellement à la séquence d'acides aminés allant de G à H sur les figures 4(a), (b) et (c) ;

une séquence d'ADN codant un polypeptide qui a une activité enzymatique de conversion du pyrophosphate de géranylgéranyle servant de substrat en un composé caroténoïde suivant dans la biosynthèse des caroténoïdes et dont la séquence d'acides aminés correspond essentiellement à la séquence d'acides aminés allant de I à J sur les figures 5(a) et (b) ; et

une séquence d'ADN codant un polypeptide qui a une activité enzymatique de conversion du β -carotène en zéaxanthine dans la biosynthèse des caroténoïdes et dont la séquence d'acides aminés correspond essentiellement à la séquence d'acides aminés allant de K à L sur la figure 6.

2. Séquence d'ADN selon la revendication 1, qui code un polypeptide enzymatique qui participe à une étape antérieure à la phase phytoène de la biosynthèse des caroténoïdes, et dont la séquence d'acides aminés correspond essentiellement à la séquence d'acides aminés allant de A à B sur les figures 1(a) et (b).

3. Séquence d'ADN selon la revendication 1, qui code un polypeptide ayant une activité enzymatique de conversion de la zéaxantine en zéaxantine-diglucoside dans la biosynthèse des caroténoïdes et dont la séquence d'acides aminés correspond essentiellement à la séquence d'acides aminés allant de C à D sur les figures 2(a) et (b).
4. Séquence d'ADN selon la revendication 1, qui code un polypeptide ayant une activité enzymatique de conversion du lycopène en β -carotène dans la biosynthèse des caroténoïdes et dont la séquence d'acides aminés correspond essentiellement à la séquence d'acides aminés allant de E à F sur les figures 3(a) et (b).
5. Séquence d'ADN selon la revendication 1, qui code un polypeptide ayant une activité enzymatique de conversion du phytoène en lycopène dans la biosynthèse des caroténoïdes, et dont la séquence d'acides aminés correspond essentiellement à la séquence d'acides aminés allant de G à H sur les figures 4(a), (b) et (c).
6. Séquence d'ADN selon la revendication 1, qui code un polypeptide ayant une activité enzymatique de conversion du pyrophosphate de géranylgéranyle servant de substrat en un composé caroténoïde suivant dans la biosynthèse des caroténoïdes et dont la séquence d'acides aminés correspond essentiellement à la séquence d'acides aminés allant de I à J sur les figures 5(a) et (b).
7. Séquence d'ADN selon la revendication 1, qui code un polypeptide ayant une activité enzymatique de conversion du β -carotène en zéaxantine dans la biosynthèse des caroténoïdes et dont la séquence d'acides aminés correspond essentiellement à la séquence d'acides aminés allant de K à L sur la figure 6.
8. Procédé pour produire un caroténoïde ou un précurseur choisi parmi l'ensemble comprenant le phytoène, le lycopène, le β -carotène, la zéaxanthine et le zéaxantine-diglucoside, caractérisé en ce qu'on transforme un hôte avec au moins l'un des ADN choisis parmi les séquences d'ADN ci-après codant les polypeptides enzymatiques qui participent à la biosynthèse des caroténoïdes par l'intermédiaire du pyrophosphate de géranylgéranyle, du phytoène et du zéaxantine-diglucoside :
 - une séquence d'ADN codant un polypeptide enzymatique qui participe à une étape préalable à la phase phytoène de la biosynthèse des caroténoïdes, et dont la séquence d'acides aminés correspond essentiellement à la séquence d'acides aminés allant de A à B sur les figures 1(a) et (b) ;
 - une séquence d'ADN codant un polypeptide qui a une activité enzymatique de conversion de la zéaxanthine en zéaxanthine-diglucoside dans la biosynthèse des caroténoïdes, et dont la séquence d'acides aminés correspond essentiellement à la séquence d'acides aminés allant de C à D sur les figures 2(a) et (b) ;
 - une séquence d'ADN codant un polypeptide qui a une activité enzymatique de conversion du lycopène en β -carotène dans la biosynthèse des caroténoïdes et dont la séquence d'acides aminés correspond essentiellement à la séquence d'acides aminés allant de E à F sur les figures 3(a) et (b) ;
 - une séquence d'ADN codant un polypeptide qui a une activité enzymatique de conversion du phytoène en lycopène dans la biosynthèse des caroténoïdes, et dont la séquence d'acides aminés correspond essentiellement à la séquence d'acides aminés allant de G à H sur les figures 4(a), (b) et (c) ;
 - une séquence d'ADN codant un polypeptide qui a une activité enzymatique de conversion du pyrophosphate de géranylgéranyle servant de substrat en un composé caroténoïde suivant dans la biosynthèse des caroténoïdes et dont la séquence d'acides aminés correspond essentiellement à la séquence d'acides aminés allant de I à J sur les figures 5(a) et (b) ; et
 - une séquence d'ADN codant un polypeptide qui a une activité enzymatique de conversion du β -carotène en zéaxantine dans la biosynthèse des caroténoïdes et dont la séquence d'acides aminés correspond essentiellement à la séquence d'acides aminés allant de K à L sur la figure 6 ;
 et en ce que l'on cultive le transformant.

230 240 250 260 270 280
 ATGACGGTCTGCGCAAAAAACACGTTTCATCTCACTCGCGATGCTGCGGAGCAGTTACTG
 MetThrValCysAlaLysLysHisValHisLeuThrArgAspAlaAlaGluGlnLeuLeu
 A

290 300 310 320 330 340
 GCTGATATTGATCGACGCTTGATCAGTTATTGCCCGTGGAGGGAGAACGGGATGTTGTG
 AlaAspIleAspArgArgLeuAspGlnLeuLeuProValGluGlyGluArgAspValVal

350 360 370 380 390 400
 GGTGCCGCGATGCGTGAAGGTGCGCTGGCACCGGAAACGTATTCGCCCCATGTTGCTG
 GlyAlaAlaMetArgGluGlyAlaLeuAlaProGlyLysArgIleArgProMetLeuLeu

410 420 430 440 450 460
 TTGCTGACCGCCCGCGATCTGGGTTGCGCTGTCAGCCATGACGGATTACTGGATTTGGCC
 LeuLeuThrAlaArgAspLeuGlyCysAlaValSerHisAspGlyLeuLeuAspLeuAla

470 480 490 500 510 520
 TGTGCGGTGGAATGGTCCACGCGGCTTCGCTGATCCTTGACGATATGCCCTGCATGGAC
 CysAlaValGluMetValHisAlaAlaSerLeuIleLeuAspAspMetProCysMetAsp

530 540 550 560 570 580
 GATGCGAAGCTGCGGCGCGGACGCCCTACCATTCATTCTCATTACGGAGAGCATGTGGCA
 AspAlaLysLeuArgArgGlyArgProThrIleHisSerHisTyrGlyGluHisValAla

590 600 610 620 630 640
 ATACTGGCGGCGGTTGCCTTGCTGAGTAAAGCCTTTGGCGTAATTGCCGATGCAGATGGC
 IleLeuAlaAlaValAlaLeuLeuSerLysAlaPheGlyValIleAlaAspAlaAspGly

650 660 670 680 690 700
 CTCACGCCGCTGGCAAAAAATCGGGCGGTTTCTGAACTGTCAAACGCCATCGGCATGCAA
 LeuThrProLeuAlaLysAsnArgAlaValSerGluLeuSerAsnAlaIleGlyMetGln

710 720 730 740 750 760
 GGATTGGTTCAGGGTCAGTTCAAGGATCTGTCTGAAGGGGATAAGCCGCGCAGCGCTGAA
 GlyLeuValGlnGlyGlnPheLysAspLeuSerGluGlyAspLysProArgSerAlaGlu

770 780 790 800 810 820
 GCTATTTTGATGACGAATCACTTTAAAACCAGCACGCTGTTTTGTGCCTCCATGCAGATG
 AlaIleLeuMetThrAsnHisPheLysThrSerThrLeuPheCysAlaSerMetGlnMet

830 840 850 860 870 880
 GCCTCGATTGTTGCGAATGCCTCCAGCGAAGCGCGTGATTGCCTGCATCGTTTTTCACTT
 AlaSerIleValAlaAsnAlaSerSerGluAlaArgAspCysLeuHisArgPheSerLeu

FIG. 1 (a)

890 900 910 920 930 940
GATCTTGGTCAGGCATTTCAACTGCTGGACGATTTGACCGATGGCATGACCGACACCGGT
AspLeuGlyGlnAlaPheGlnLeuLeuAspAspLeuThrAspGlyMetThrAspThrGly

950 960 970 980 990 1000
AAGGATAGCAATCAGGACGCCGGTAAATCGACGCTGGTCAATCTGTTAGGCCCGAGGGCG
LysAspSerAsnGlnAspAlaGlyLysSerThrLeuValAsnLeuLeuGlyProArgAla

1010 1020 1030 1040 1050 1060
GTTGAAGAACGTCTGAGACAACATCTTCAGCTTGCCAGTGAGCATCTCTCTGCGGCCTGC
ValGluGluArgLeuArgGlnHisLeuGlnLeuAlaSerGluHisLeuSerAlaAlaCys

1070 1080 1090 1100 1110 1120
CAACACGGGCACGCCACTCAACATTTTATTCAGGCCTGGTTTGACAAAAAACTCGCTGCC
GlnHisGlyHisAlaThrGlnHisPheIleGlnAlaTrpPheAspLysLysLeuAlaAla

1130
GTCAGTTAA
ValSer***

↑
B

FIG. 1 (b)

1150 1160 1170 1180 1190 1200
 ATGAGCCATTTTCGCGGCGATCGCACCGCCTTTTTACAGCCATGTTTCGCGCATTACAGAAT
 MetSerHisPheAlaAlaIleAlaProProPheTyrSerHisValArgAlaLeuGlnAsn
 ↑
 C

1210 1220 1230 1240 1250 1260
 CTCGCTCAGGAACTGGTCGCGCGCGGTTCATCGGGTGACCTTTATTTCAGCAATACGATATT
 LeuAlaGlnGluLeuValAlaArgGlyHisArgValThrPheIleGlnGlnTyrAspIle

1270 1280 1290 1300 1310 1320
 AAACACTTGATCGATAGCGAAACCATTGGATTTCATTCCGTCGGGACAGACAGCCATCCC
 LysHisLeuIleAspSerGluThrIleGlyPheHisSerValGlyThrAspSerHisPro

1330 1340 1350 1360 1370 1380
 CCCGGCGCGTTAACGCGCGTGCTACACCTGGCGGCTCATCCTCTGGGGCCGTCAATGCTG
 ProGlyAlaLeuThrArgValLeuHisLeuAlaAlaHisProLeuGlyProSerMetLeu

1390 1400 1410 1420 1430 1440
 AAGCTCATCAATGAAATGGCGCGCACCAACCGATATGCTGTGCCGCGAACTCCCCAGGCA
 LysLeuIleAsnGluMetAlaArgThrThrAspMetLeuCysArgGluLeuProGlnAla

1450 1460 1470 1480 1490 1500
 TTTAACGATCTGGCCGTCGATGGCGTCATTGTTGATCAAATGGAACCGGCAGGCGCGCTC
 PheAsnAspLeuAlaValAspGlyValIleValAspGlnMetGluProAlaGlyAlaLeu

1510 1520 1530 1540 1550 1560
 GTTGCTGAAGCACTGGGACTGCCGTTTATCTCTGTGCGCTGCGCGCTGCCTCTCAATCGT
 ValAlaGluAlaLeuGlyLeuProPheIleSerValAlaCysAlaLeuProLeuAsnArg

1570 1580 1590 1600 1610 1620
 GAACCGGATATGCCCTGGCGGTTATGCCTTTTGAATACGGGACCAGCGACGCGGCTCGC
 GluProAspMetProLeuAlaValMetProPheGluTyrGlyThrSerAspAlaAlaArg

1630 1640 1650 1660 1670 1680
 GAACGTTATGCCGCCAGTGAAAAATTTATGACTGGCTAATGCGTCGTCATGACCGTGTC
 GluArgTyrAlaAlaSerGluLysIleTyrAspTrpLeuMetArgArgHisAspArgVal

1690 1700 1710 1720 1730 1740
 ATTGCCGAACACAGCCACAGAATGGGCTTAGCCCCCGGCAAAGCTTCACCAAGTGTTTT
 IleAlaGluHisSerHisArgMetGlyLeuAlaProArgGlnLysLeuHisGlnCysPhe

1750 1760 1770 1780 1790 1800
 TCGCCACTGGCGCAAATCAGCCAGCTTGTTTCCTGAACTGGATTTTCCCCGCAAAGCGTTA
 SerProLeuAlaGlnIleSerGlnLeuValProGluLeuAspPheProArgLysAlaLeu

FIG. 2 (a)

1810 1820 1830 1840 1850 1860
 CCGGCTTGTTCATGCCGTCGGGCCTCTGCGCGAAACGCACGCACCGTCAACGTCTTCA
 ProAlaCysPheHisAlaValGlyProLeuArgGluThrHisAlaProSerThrSerSer

1870 1880 1890 1900 1910 1920
 TCCCGTTATTTTACATCCTCAGAAAAACCCCGGATTTTCGCCTCGCTGGGCACGCTTCAG
 SerArgTyrPheThrSerSerGluLysProArgIlePheAlaSerLeuGlyThrLeuGln

1930 1940 1950 1960 1970 1980
 GGACACCGTTATGGGCTGTTTAAAACGATAGTGAAAGCCTGTGAAGAAATTGACGGTCAG
 GlyHisArgTyrGlyLeuPheLysThrIleValLysAlaCysGluGluIleAspGlyGln

1990 2000 2010 2020 2030 2040
 CTCCTGTTAGCCCACTGTGGTCGTCTTACGGACTCTCAGTGTGAAGAGCTGGCGCGAAGC
 LeuLeuLeuAlaHisCysGlyArgLeuThrAspSerGlnCysGluGluLeuAlaArgSer

2050 2060 2070 2080 2090 2100
 CGTCATACACAGGTGGTGGATTTTGCCGATCAGTCAGCCGCGCTGTCTCAGGCGCAGCTG
 ArgHisThrGlnValValAspPheAlaAspGlnSerAlaAlaLeuSerGlnAlaGlnLeu

2110 2120 2130 2140 2150 2160
 GCGATCACCCACGGCGGCATGAATACGGTACTGGACGCGATTAATTACCGGACGCCCCTT
 AlaIleThrHisGlyGlyMetAsnThrValLeuAspAlaIleAsnTyrArgThrProLeu

2170 2180 2190 2200 2210 2220
 TTAGCGCTTCCGCTGGCCTTTGATCAGCCCGGCGTCGCGTCACGCATCGTTTATCACGGC
 LeuAlaLeuProLeuAlaPheAspGlnProGlyValAlaSerArgIleValTyrHisGly

2230 2240 2250 2260 2270 2280
 ATCGGCAAGCGTGCTTCCCGCTTTACCACCAGCCATGCTTTGGCTCGTCAGATGCGTTCA
 IleGlyLysArgAlaSerArgPheThrThrSerHisAlaLeuAlaArgGlnMetArgSer

2290 2300 2310 2320 2330 2340
 TTGCTGACCAACGTCGACTTTCAGCAGCGCATGGCGAAAATCCAGACAGCCCTTCGTTTG
 LeuLeuThrAsnValAspPheGlnGlnArgMetAlaLysIleGlnThrAlaLeuArgLeu

2350 2360 2370 2380 2390 2400
 GCAGGGGGCACCATGGCCGCTGCCGATATCATTGAGCAGGTTATGTGCACCGGTCAGCCT
 AlaGlyGlyThrMetAlaAlaAlaAspIleIleGluGlnValMetCysThrGlyGlnPro

2410 2420 2430
 GTCCTTAAGTGGGAGCGGCTATGCAACCGCATTATGA
 ValLeuSerGlySerGlyTyrAlaThrAlaLeu***

D
↓

FIG. 2 (b)

2430 2440 2450 2460 2470 2480
 ATGCAACCGCATTATGATCTGATTCTCGTGGGGGCTGGACTCGCGAATGGCCTTATCGCC
 MetGlnProHisTyrAspLeuIleLeuValGlyAlaGlyLeuAlaAsnGlyLeuIleAla
 ↑
 E 2490 2500 2510 2520 2530 2540
 CTGCGTCTTCAGCAGCAGCAACCTGATATGCGTATTTTGCTTATCGACGCCGCACCCAG
 LeuArgLeuGlnGlnGlnGlnProAspMetArgIleLeuLeuIleAspAlaAlaProGln
 2550 2560 2570 2580 2590 2600
 GCGGGCGGGAATCATACGTGGTCATTTACACACGATGATTTGACTGAGAGCCAACATCGT
 AlaGlyGlyAsnHisThrTrpSerPheHisHisAspAspLeuThrGluSerGlnHisArg
 2610 2620 2630 2640 2650 2660
 TGGATAGCTCCGCTGGTGGTTCATCACTGGCCCGACTATCAGGTACGCTTTCCACACGC
 TrpIleAlaProLeuValValHisHisTrpProAspTyrGlnValArgPheProThrArg
 2670 2680 2690 2700 2710 2720
 CGTCGTAAGCTGAACAGCGGCTACTTTTGTATTACTTCTCAGCGTTTCGCTGAGGTTTTA
 ArgArgLysLeuAsnSerGlyTyrPheCysIleThrSerGlnArgPheAlaGluValLeu
 2730 2740 2750 2760 2770 2780
 CAGCGACAGTTTGGCCCGCACTTGTGGATGGATACCGCGGTTCGAGAGGTTAATGCGGAA
 GlnArgGlnPheGlyProHisLeuTrpMetAspThrAlaValAlaGluValAsnAlaGlu
 2790 2800 2810 2820 2830 2840
 TCTGTTCGGTTGAAAAAGGGTCAGGTTATCGGTGCCCGCGCGGTGATTGACGGGCGGGGT
 SerValArgLeuLysLysGlyGlnValIleGlyAlaArgAlaValIleAspGlyArgGly
 2850 2860 2870 2880 2890 2900
 TATGCGGCAAATTCAGCACTGAGCGTGGGCTTCCAGGCGTTTATTGGCCAGGAATGGCGA
 TyrAlaAlaAsnSerAlaLeuSerValGlyPheGlnAlaPheIleGlyGlnGluTrpArg
 2910 2920 2930 2940 2950 2960
 TTGAGCCACCCGCATGGTTTATCGTCTCCATTATCATGGATGCCACGGTCGATCAGCAA
 LeuSerHisProHisGlyLeuSerSerProIleIleMetAspAlaThrValAspGlnGln
 2970 2980 2990 3000 3010 3020
 AATGGTTATCGCTTCGTGTACAGCCTGCCGCTCTCGCCGACCAGATTGTTAATTGAAGAC
 AsnGlyTyrArgPheValTyrSerLeuProLeuSerProThrArgLeuLeuIleGluAsp
 3030 3040 3050 3060 3070 3080
 ACGCACTATATTGATAATGCGACATTAGATCCTGAATGCGCGCGGCAAAATATTTGCGAC
 ThrHisTyrIleAspAsnAlaThrLeuAspProGluCysAlaArgGlnAsnIleCysAsp

FIG. 3 (a)

3090 3100 3110 3120 3130 3140
 TATGCCGCGCAACAGGGTTGGCAGCTTCAGACACTGCTGCGAGAAGAACAGGGCGCCTTA
 TyrAlaAlaGlnGlnGlyTrpGlnLeuGlnThrLeuLeuArgGluGluGlnGlyAlaLeu

3150 3160 3170 3180 3190 3200
 CCCATTACTCTGTTCGGGCAATGCCGACGCATTCTGGCAGCAGCGCCCCCTGGCCTGTAGT
 ProlleThrLeuSerGlyAsnAlaAspAlaPheTrpGlnGlnArgProLeuAlaCysSer

3210 3220 3230 3240 3250 3260
 GGATTACGTGCCGGTCTGTTCCATCCTACCACCGGCTATTCACTGCCGCTGGCGGTTGCC
 GlyLeuArgAlaGlyLeuPheHisProThrThrGlyTyrSerLeuProLeuAlaValAla

3270 3280 3290 3300 3310 3320
 GTGGCCGACCGCCTGAGTGCACCTTGATGTCTTTACGTCCGCCTCAATTCACCATGCCATT
 ValAlaAspArgLeuSerAlaLeuAspValPheThrSerAlaSerIleHisHisAlaIle

3330 3340 3350 3360 3370 3380
 ACGCATTTTGGCCGCGAGCGCTGGCAGCAGCAGGGCTTTTCCGCATGCTGAATCGCATG
 ThrHisPheAlaArgGluArgTrpGlnGlnGlnGlyPhePheArgMetLeuAsnArgMet

3390 3400 3410 3420 3430 3440
 CTGTTTTTAGCCGGACCCGCCGATTACGCTGGCGGGTTATGCAGCGTTTTTATGGTTTA
 LeuPheLeuAlaGlyProAlaAspSerArgTrpArgValMetGlnArgPheTyrGlyLeu

3450 3460 3470 3480 3490 3500
 CCTGAAGATTTAATTGCCCGTTTTTATGCGGGAAACTCACGCTGACCGATCGGCTACGT
 ProGluAspLeuIleAlaArgPheTyrAlaGlyLysLeuThrLeuThrAspArgLeuArg

3510 3520 3530 3540 3550 3560
 ATTCTGAGCGGCAAGCCGCCTGTTCCGGTATTAGCAGCATTGCAAGCCATTATGACGACT
 IleLeuSerGlyLysProProValProValLeuAlaAlaLeuGlnAlaIleMetThrThr

3570
 CATCGTTAA
 HisArg***
 ↑
 F

FIG. 3 (b)

3590 3600 3610 3620 3630 3640
 ATGAAACCAACTACGGTAATTGGTGCAGGCTTCGGTGGCCTGGCACTGGCAATTCGTCTA
 MetLysProThrThrValIleGlyAlaGlyPheGlyGlyLeuAlaLeuAlaIleArgLeu
 ↑
 G 3650 3660 3670 3680 3690 3700
 CAAGCTGCGGGGATCCCCGTCTTACTGCTTGAACAACGTGATAAACCCGGCGGTCTGGGCT
 GlnAlaAlaGlyIleProValLeuLeuLeuGluGlnArgAspLysProGlyGlyArgAla

 3710 3720 3730 3740 3750 3760
 TATGTCTACGAGGATCAGGGGTTTACCTTTGATGCAGGCCCGACGGTTATCACCGATCCC
 TyrValTyrGluAspGlnGlyPheThrPheAspAlaGlyProThrValIleThrAspPro

 3770 3780 3790 3800 3810 3820
 AGTGCCATTGAAGAACTGTTTGCAGTGGCAGGAAAACAGTTAAAAGAGTATGTCTGAAGT
 SerAlaIleGluGluLeuPheAlaLeuAlaGlyLysGlnLeuLysGluTyrValGluLeu

 3830 3840 3850 3860 3870 3880
 CTGCCGGTTACGCCGTTTTACCGCCTGTGTTGGGAGTCAGGGAAGGTCTTTAATTACGAT
 LeuProValThrProPheTyrArgLeuCysTrpGluSerGlyLysValPheAsnTyrAsp

 3890 3900 3910 3920 3930 3940
 AACGATCAAACCCGGCTCGAAGCGCAGATTTCAGCAGTTTAAATCCCCGCGATGTCTGAAGGT
 AsnAspGlnThrArgLeuGluAlaGlnIleGlnGlnPheAsnProArgAspValGluGly

 3950 3960 3970 3980 3990 4000
 TATCGTCAGTTTCTGGACTATTCACGCGCGGTGTTTAAAGAAGGCTATCTAAAGCTCGGT
 TyrArgGlnPheLeuAspTyrSerArgAlaValPheLysGluGlyTyrLeuLysLeuGly

 4010 4020 4030 4040 4050 4060
 ACTGTCCCTTTTTTATCGTTTCAGAGACATGCTTCGCGCCGCACCTCAACTGGCGAAACTG
 ThrValProPheLeuSerPheArgAspMetLeuArgAlaAlaProGlnLeuAlaLysLeu

 4070 4080 4090 4100 4110 4120
 CAGGCATGGAGAAGCGTTTACAGTAAGGTTGCCAGTTACATCGAAGATGAACATCTGCGC
 GlnAlaTrpArgSerValTyrSerLysValAlaSerTyrIleGluAspGluHisLeuArg

 4130 4140 4150 4160 4170 4180
 CAGGCGTTTTCTTTCCACTCGCTGTTGGTGGGCGGCAATCCCTTCGCCACCTCATCCATT
 GlnAlaPheSerPheHisSerLeuLeuValGlyGlyAsnProPheAlaThrSerSerIle

 4190 4200 4210 4220 4230 4240
 TATACGTTGATACACGCGCTGGAGCGTGAGTGGGGCGTCTGGTTTCCGCGTGGCGGCACC
 TyrThrLeuIleHisAlaLeuGluArgGluTrpGlyValTrpPheProArgGlyGlyThr

FIG. 4 (a)

4250 4260 4270 4280 4290 4300
 GGCGCATTAGTTCAGGGGATGATAAAGCTGTTTCAGGATCTGGGTGGCGAAGTCGTGTTA
 GlyAlaLeuValGlnGlyMetIleLysLeuPheGlnAspLeuGlyGlyGluValValLeu

4310 4320 4330 4340 4350 4360
 AACGCCAGAGTCAGCCATATGGAAACGACAGGAAACAAGATTGAAGCCGTGCATTTAGAG
 AsnAlaArgValSerHisMetGluThrThrGlyAsnLysIleGluAlaValHisLeuGlu

4370 4380 4390 4400 4410 4420
 GACGGTCGCAGGTTCTGACGCAAGCCGTGCGCTCAAATGCAGATGTGGTTCATACCTAT
 AspGlyArgArgPheLeuThrGlnAlaValAlaSerAsnAlaAspValValHisThrTyr

4430 4440 4450 4460 4470 4480
 CGCGACCTGTAAAGCCAGCACCTGCCGCGGTTAAGCAGTCCAACAACTGCAGACTAAG
 ArgAspLeuLeuSerGlnHisProAlaAlaValLysGlnSerAsnLysLeuGlnThrLys

4490 4500 4510 4520 4530 4540
 CGCATGAGTAACTCTCTGTTTGTGCTCTATTTTGGTTTGAATCACCATCATGATCAGCTC
 ArgMetSerAsnSerLeuPheValLeuTyrPheGlyLeuAsnHisHisHisAspGlnLeu

4550 4560 4570 4580 4590 4600
 GCGCATCACACGTTTTGTTTCGGCCCGCGTTACCGCGAGCTGATTGACGAAATTTTAAAT
 AlaHisHisThrValCysPheGlyProArgTyrArgGluLeuIleAspGluIlePheAsn

4610 4620 4630 4640 4650 4660
 CATGATGGCCTCGCAGAGGACTTCTCACTTTATCTGCACGCGCCCTGTGTACAGGATTCTG
 HisAspGlyLeuAlaGluAspPheSerLeuTyrLeuHisAlaProCysValThrAspSer

4670 4680 4690 4700 4710 4720
 TCACTGGCGCCTGAAGGTTGCGGCAGTTACTATGTGTTGGCGCCGGTGCCGCATTTAGGC
 SerLeuAlaProGluGlyCysGlySerTyrTyrValLeuAlaProValProHisLeuGly

4730 4740 4750 4760 4770 4780
 ACCGCGAACCTCGACTGGACGTTGAGGGGCCAAACTACGCGACCGTATTTTTGCGTAC
 ThrAlaAsnLeuAspTrpThrValGluGlyProLysLeuArgAspArgIlePheAlaTyr

4790 4800 4810 4820 4830 4840
 CTTGAGCAGCATTACATGCCTGGCTTACGGAGTCAGCTGGTCACGCACCGGATGTTTACG
 LeuGluGlnHisTyrMetProGlyLeuArgSerGlnLeuValThrHisArgMetPheThr

4850 4860 4870 4880 4890 4900
 CCGTTTGATTTTCGCGACCAGCTTAATGCCTATCATGGCTCAGCCTTTTCTGTGGAGCCC
 ProPheAspPheArgAspGlnLeuAsnAlaTyrHisGlySerAlaPheSerValGluPro

FIG. 4 (b)

4910 4920 4930 4940 4950 4960
GTTCTTACCCAGAGCGCCTGGTTTCGGCCGCATAACCGCGATAAAACCATTACTAATCTC
ValLeuThrGlnSerAlaTrpPheArgProHisAsnArgAspLysThrIleThrAsnLeu

4970 4980 4990 5000 5010 5020
TACCTGGTCGGCGCAGGCACGCATCCCGGCGCAGGCATTCCTGGCGTCATCGGCTCGGCA
TyrLeuValGlyAlaGlyThrHisProGlyAlaGlyIleProGlyValIleGlySerAla

5030 5040 5050 5060
AAAGCGACAGCAGGTTTGATGCTGGAGGATCTGATTTGA
LysAlaThrAlaGlyLeuMetLeuGluAspLeuIle***
↑
H

FIG. 4 (c)

5100 5110 5120 5130 5140 5150
 ATGGCAGTTGGCTCGAAAAGTTTTGCGACAGCCTCAAAGTTATTTGATGCAAAAACCCGG
 MetAlaValGlySerLysSerPheAlaThrAlaSerLysLeuPheAspAlaLysThrArg

5160 5170 5180 5190 5200 5210
 CGCAGCGTACTGATGCTCTACGCCTGGTGCCGCCATTGTGACGATGTTATTGACGATCAG
 ArgSerValLeuMetLeuTyrAlaTrpCysArgHisCysAspAspValIleAspAspGln

5220 5230 5240 5250 5260 5270
 ACGCTGGGCTTTCAGGCCCGGCAGCCTGCCTTACAAACGCCCGAACAACGTCTGATGCAA
 ThrLeuGlyPheGlnAlaArgGlnProAlaLeuGlnThrProGluGlnArgLeuMetGln

5280 5290 5300 5310 5320 5330
 CTTGAGATGAAAACGCGCCAGGCCTATGCAGGATCGCAGATGCACGAACCGGCGTTTGCG
 LeuGluMetLysThrArgGlnAlaTyrAlaGlySerGlnMetHisGluProAlaPheAla

5340 5350 5360 5370 5380 5390
 GCTTTTCAGGAAGTGGCTATGGCTCATGATATCGCCCCGGCTTACGCGTTTGATCATCTG
 AlaPheGlnGluValAlaMetAlaHisAspIleAlaProAlaTyrAlaPheAspHisLeu

5400 5410 5420 5430 5440 5450
 GAAGGCTTCGCCATGGATGTACGCGAAGCGCAATACAGCCAACTGGATGATACGCTGCGC
 GluGlyPheAlaMetAspValArgGluAlaGlnTyrSerGlnLeuAspAspThrLeuArg

5460 5470 5480 5490 5500 5510
 TATTGCTATCACGTTGCAGGCGTTGTCTGGCTTGATGATGGCGCAAATCATGGGCGTGCGG
 TyrCysTyrHisValAlaGlyValValGlyLeuMetMetAlaGlnIleMetGlyValArg

5520 5530 5540 5550 5560 5570
 GATAACGCCACGCTGGACCGCGCCTGTGACCTTGGGCTGGCATTTCAGTTGACCAATATT
 AspAsnAlaThrLeuAspArgAlaCysAspLeuGlyLeuAlaPheGlnLeuThrAsnIle

5580 5590 5600 5610 5620 5630
 GCTCGCGATATTGTGGACGATGCGCATGCGGGCCGCTGTTATCTGCCGGCAAGCTGGCTG
 AlaArgAspIleValAspAspAlaHisAlaGlyArgCysTyrLeuProAlaSerTrpLeu

5640 5650 5660 5670 5680 5690
 GAGCATGAAGGTCTGAACAAAGAGAATTATGCGGCACCTGAAAACCGTCAGGCGCTGAGC
 GluHisGluGlyLeuAsnLysGluAsnTyrAlaAlaProGluAsnArgGlnAlaLeuSer

5700 5710 5720 5730 5740 5750
 CGTATCGCCCGTCGTTTGGTGCAGGAAGCAGAACCTTACTATTTGTCTGCCACAGCCGGC
 ArgIleAlaArgArgLeuValGlnGluAlaGluProTyrTyrLeuSerAlaThrAlaGly

FIG. 5 (a)

5760 5770 5780 5790 5800 5810
CTGGCAGGGTTGCCCCTGCGTTCCGCCTGGGCAATCGCTACGGCGAAGCAGGTTTACCGG
LeuAlaGlyLeuProLeuArgSerAlaTrpAlaIleAlaThrAlaLysGlnValTyrArg

5820 5830 5840 5850 5860 5870
AAAATAGGTGTCAAAGTTGAACAGGCCGGTCAGCAAGCCTGGGATCAGCGGCAGTCAACG
LysIleGlyValLysValGluGlnAlaGlyGlnGlnAlaTrpAspGlnArgGlnSerThr

5880 5890 5900 5910 5920 5930
ACCACGCCCGAAAAATTAACGCTGCTGCTGGCCGCCTCTGGTCAGGCCCTTACTTCCCGG
ThrThrProGluLysLeuThrLeuLeuLeuAlaAlaSerGlyGlnAlaLeuThrSerArg

5940 5950 5960 5970 5980
ATGCGGGCTCATCCTCCCCGCCCTGCGCATCTCTGGCAGCGCCCGCTCTAG
MetArgAlaHisProProArgProAlaHisLeuTrpGlnArgProLeu***

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J

FIG. 5 (b)

6452

ATGTTGTGGATTTGGAATGCCCTGATCGTTTTCGTTACCGTGATTGGCATGGAAGTGATT
 MetLeuTrpIleTrpAsnAlaLeuIleValPheValThrValIleGlyMetGluValIle

K

GCTGCACTGGCACACAAATACATCATGCACGGCTGGGGTTGGGGATGGCATCTTTCACAT
 AlaAlaLeuAlaHisLysTyrIleMetHisGlyTrpGlyTrpGlyTrpHisLeuSerHis

CATGAACCGCGTAAAGGTGCGTTTGAAGTTAACGATCTTTATGCCGTGGTTTTTGGCTGCA
 HisGluProArgLysGlyAlaPheGluValAsnAspLeuTyrAlaValValPheAlaAla

TTATCGATCCTGCTGATTTATCTGGGCAGTACAGGAATGTGGCCGCTCCAGTGGATTGGC
 LeuSerIleLeuLeuIleTyrLeuGlySerThrGlyMetTrpProLeuGlnTrpIleGly

GCAGGTATGACGGCGTATGGATTACTCTATTTTATGGTGCACGACGGGCTGGTGCATCAA
 AlaGlyMetThrAlaTyrGlyLeuLeuTyrPheMetValHisAspGlyLeuValHisGln

CGTTGGCCATTCCGCTATATTCCACGCAAGGGCTACCTCAAACGGTTGTATATGGCGCAC
 ArgTrpProPheArgTyrIleProArgLysGlyTyrLeuLysArgLeuTyrMetAlaHis

CGTATGCATCACGCCGTCAGGGGCAAAGAAGGTTGTGTTTCTTTTGGCTTCCTCTATGCG
 ArgMetHisHisAlaValArgGlyLysGluGlyCysValSerPheGlyPheLeuTyrAla

CCGCCCCTGTCAAACTTCAGGCGACGCTCCGGGAAAGACATGGCGCTAGAGCGGGCGCT
 ProProLeuSerLysLeuGlnAlaThrLeuArgGluArgHisGlyAlaArgAlaGlyAla

GCCAGAGATGCGCAGGGCGGGGAGGATGAGCCCGCATCCGGGAAGTAA
 AlaArgAspAlaGlnGlyGlyGluAspGluProAlaSerGlyLys***

5925

↑
L

FIG. 6

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1      10      20      30      40      50
GGTACCGCAC GGTCTGCCAA TCCGACGGAG GTTTATGAAT TTTCCACCTT TTCCACAAGC

      70      80      90      100      110
TCAACTAGTA TTAACGATGT GGATTTAGCA AAAAAAACCT GTAACCCTAA ATGTAAAATA

      130      140      150      160      170
ACGGGTAAGC CTGCCAACCA TGTTATGGCA GATTAAGCGT CTTTTTGAAG GGCACCGCAT

      190      200      210      220      230
CTTTCGCGTT GCCGTAAATG TATCCGTTTA TAAGGACAGC CCGAATGACG GTCTGCGCAA
                        A
      250      260      270      280      290
AAAAACACGT TCATCTCACT CGCGATGCTG CGGAGCAGTT ACTGGCTGAT ATTGATCGAC

      310      320      330      340      350
GCCTTGATCA GTTATTGCCC GTGGAGGGAG AACGGGATGT TGTGGGTGCC GCGATGCGTG

      370      380      390      400      410
AAGGTGCGCT GGCACCGGGA AAACGTATTC GCCCATGTT GCTGTTGCTG ACCGCCCCGG

      430      440      450      460      470
ATCTGGGTTG CGCTGTCAGC CATGACGGAT TACTGGATTT GGCCTGTGCG GTGGAAATGG

      490      500      510      520      530
TCCACGCGGC TTCGCTGATC CTTGACGATA TGCCCTGCAT GGACGATGCG AAGCTGCGGC

      550      560      570      580      590
GCGGACGCCC TACCATTTCAT TCTCATTACG GAGAGCATGT GGCAATACTG GCGGCGGTTG

      610      620      630      640      650
CCTTGCTGAG TAAAGCCTTT GGCGTAATTG CCGATGCAGA TGGCCTCACG CCGCTGGCAA

      670      680      690      700      710
AAAATCGGGC GGTTCCTGAA CTGTCAAACG CCATCGGCAT GCAAGGATTG GTTCAGGGTC

      730      740      750      760      770
AGTTCAAGGA TCTGTCTGAA GGGGATAAGC CGCGCAGCGC TGAAGCTATT TTGATGACGA

      790      800      810      820      830
ATCACTTTAA AACCAGCACG CTGTTTTGTG CCTCCATGCA GATGGCCTCG ATTGTTGCGA

      850      860      870      880      890
ATGCCTCCAG CGAAGCGCGT GATTGCCTGC ATCGTTTTTC ACTTGATCTT GGTCAGGCAT

      910      920      930      940      950
TTCAACTGCT GGACGATTTG ACCGATGGCA TGACCGACAC CGGTAAGGAT AGCAATCAGG

      970      980      990      1000      1010
ACGCCGGTAA ATCGACGCTG GTCAATCTGT TAGGCCCGAG GGCGGTTGAA GAACGTCTGA

      1030      1040      1050      1060      1070
GACAACATCT TCAGCTTGCC AGTGAGCATC TCTCTGCGGC CTGCCAACAC GGGCACGCCA

      1090      1100      1110      1120      1130
CTCAACATTT TATTCAGGCC TGGTTTGACA AAAAATCGC TGCCGTCAGT TAAGGATGCT
                        B

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FIG. 7 (a)

C 1150 1160 1170 1180 1190
 GCATGAGCCA TTTCGCGGCG ATCGCACCGC CTTTTTACAG CCATGTTCGC GCATTACAGA
 1210 1220 1230 1240 1250
 ATCTCGCTCA GGAAC TGGTC GCGCGCGGTC ATCGGGTGAC CTTTATTCAG CAATACGATA
 1270 1280 1290 1300 1310
 TTAAACACTT GATCGATAGC GAAACCATTG GATTTCATT C GTCGGGACA GACAGCCATC
 1330 1340 1350 1360 1370
 CCCCCGCGC GTTAACGCGC GTGCTACACC TGGCGGCTCA TCCTCTGGGG CCGTCAATGC
 1390 1400 1410 1420 1430
 TGAAGCTCAT CAATGAAATG GCGCGCACCA CCGATATGCT GTGCCGCGAA CTCCCCCAGG
 1450 1460 1470 1480 1490
 CATTTAACGA TCTGGCCGTC GATGGCGTCA TTGTTGATCA AATGGAACCG GCAGGCGCGC
 1510 1520 1530 1540 1550
 TCGTTGCTGA AGCACTGGGA CTGCCGTTA TCTCTGTCGC CTGCGCGCTG CCTCTCAATC
 1570 1580 1590 1600 1610
 GTGAACCGGA TATGCCCTG GCGGTTATGC CTTTCGAATA CGGGACCAGC GACGCGGCTC
 1630 1640 1650 1660 1670
 GCGAACGTTA TGCCGCCAGT GAAAAAATTT ATGACTGGCT AATGCGTCGT CATGACCGTG
 1690 1700 1710 1720 1730
 TCATTGCCGA ACACAGCCAC AGAATGGGCT TAGCCCCCG GCAAAAGCTT CACCAGTGTT
 1750 1760 1770 1780 1790
 TTTCGCCACT GGC GCAAATC AGCCAGCTTG TTCCTGAACT GGATTTTCCC CGCAAAGCGT
 1810 1820 1830 1840 1850
 TACCGGCTTG TTTTCATGCC GTCGGGCCTC TGC GCGAAAC GCACGCACCG TCAACGTCTT
 1870 1880 1890 1900 1910
 CATCCCGTTA TTTTACATCC TCAGAAAAAC CCCGATTTT CGCCTCGCTG GGCACGCTTC
 1930 1940 1950 1960 1970
 AGGGACACCG TTATGGGCTG TTTAAACGA TAGTGAAAGC CTGTGAAGAA ATTGACGGTC
 1990 2000 2010 2020 2030
 AGCTCCTGTT AGCCCACTGT GGTCGTCTTA CGGACTCTCA GTGTGAAGAG CTGGCGCGAA
 2050 2060 2070 2080 2090
 GCCGTCATAC ACAGGTGGTG GATTTTGCCG ATCAGTCAGC CGCGCTGTCT CAGGCGCAGC
 2110 2120 2130 2140 2150
 TGGCGATCAC CCACGGCGGC ATGAATACGG TACTGGACGC GATTAATTAC CGGACGCCCC
 2170 2180 2190 2200 2210
 TTTTAGCGCT TCCGCTGGCC TTTGATCAGC CCGGCGTCGC GTCACGCATC GTTTATCACG
 2230 2240 2250 2260 2270
 GCATCGGCAA GCGTGCTTCC CGCTTTACCA CCAGCCATGC TTTGGCTCGT CAGATGCGTT

FIG. 7 (b)

2290	2300	2310	2320	2330
CATTGCTGAC	CAACGTCGAC	TTTCAGCAGC	GCATGGCGAA	AATCCAGACA
				GCCCTTCGTT
2350	2360	2370	2380	2390
TGGCAGGGGG	CACCATGGCC	GCTGCCGATA	TCATTGAGCA	GGTTATGTGC
				ACCGGTCAGC
2410	2420	2430	2440	2450
CTGTCTTAAG	TGGGAGCGGC	TATGCAACCG	CATTATGATC	TGATTCTCGT
				GGGGGCTGGA
2470	2480	2490	2500	2510
CTCGCGAATG	GCCTTATCGC	CCTGCGTCTT	CAGCAGCAGC	AACCTGATAT
				GCGTATTTTG
2530	2540	2550	2560	2570
CTTATCGACG	CCGCACCCCA	GGCGGGCGGG	AATCATACTG	GGTCATTTC
				CCACGATGAT
2590	2600	2610	2620	2630
TTGACTGAGA	GCCAACATCG	TTGGATAGCT	CCGCTGGTGG	TTCATCACTG
				GCCCGACTAT
2650	2660	2670	2680	2690
CAGGTACGCT	TTCCACACG	CCGTCGTAAG	CTGAACAGCG	GCTACTTTTG
				TATTACTTCT
2710	2720	2730	2740	2750
CAGCGTTTCG	CTGAGGTTT	ACAGCGACAG	TTTGGCCCGC	ACTTGTGGAT
				GGATACCGCG
2770	2780	2790	2800	2810
GTCGCAGAGG	TTAATGCGGA	ATCTGTTCGG	TTGAAAAGG	GTCAGGTTAT
				CGGTGCCCCG
2830	2840	2850	2860	2870
GCGGTGATTG	ACGGGCGGGG	TTATGCGGCA	AATTCAGCAC	TGAGCGTGGG
				CTTCCAGGCG
2890	2900	2910	2920	2930
TTTATTGGCC	AGGAATGGCG	ATTGAGCCAC	CCGCATGGTT	TATCGTCTCC
				CATTATCATG
2950	2960	2970	2980	2990
GATGCCACGG	TCGATCAGCA	AAATGGTTAT	CGCTTCGTGT	ACAGCCTGCC
				GCTCTCGCCG
3010	3020	3030	3040	3050
ACCAGATTGT	TAATTGAAGA	CACGCACTAT	ATTGATAATG	CGACATTAGA
				TCCTGAATGC
3070	3080	3090	3100	3110
GCGCGGCAAA	ATATTTGCGA	CTATGCCGCG	CAACAGGGTT	GGCAGCTTCA
				GAACTGCTG
3130	3140	3150	3160	3170
CGAGAAGAAC	AGGGCGCCTT	ACCCATTACT	CTGTCGGGCA	ATGCCGACGC
				ATTCTGGCAG
3190	3200	3210	3220	3230
CAGCGCCCCC	TGGCCTGTAG	TGGATTACGT	GCCGGTCTGT	TCCATCCTAC
				CACCGGCTAT
3250	3260	3270	3280	3290
TCACTGCCGC	TGGCGGTTGC	CGTGGCCGAC	CGCCTGAGTG	CACTTGATGT
				CTTTACGTCG
3310	3320	3330	3340	3350
GCCTCAATTC	ACCATGCCAT	TACGCATTTT	GCCCCGCGAGC	GCTGGCAGCA
				GCAGGGCTTT
3370	3380	3390	3400	3410
TTCCGCATGC	TGAATCGCAT	GCTGTTTTTA	GCCGGACCCG	CCGATTCACG
				CTGGCGGGTT

FIG. 7 (c)

3430	3440	3450	3460	3470
ATGCAGCGTT	TTTATGGTTT	ACCTGAAGAT	TTAATTGCC	GTTTTTATGC
				GGGAAAACCTC
3490	3500	3510	3520	3530
ACGCTGACCG	ATCGGCTACG	TATTCTGAGC	GGCAAGCCGC	CTGTTCCGGT
				ATTAGCAGCA
3550	3560	3570	3580	3590
TTGCAAGCCA	TTATGACGAC	TCATCGTTAA	AGAGCGACTA	CATGAAACCA
				ACTACGGTAA
3610	3620	3630	3640	3650
TTGGTGCAGG	CTTCGGTGGC	CTGGCACTGG	CAATTCGTCT	ACAAGCTGCG
				GGGATCCCCG
3670	3680	3690	3700	3710
TCTTACTGCT	TGAACAACGT	GATAAACCCG	GCGGTCGGGC	TTATGTCTAC
				GAGGATCAGG
3730	3740	3750	3760	3770
GGTTTACCTT	TGATGCAGGC	CCGACGGTTA	TCACCGATCC	CAGTGCCATT
				GAAGAACTGT
3790	3800	3810	3820	3830
TTGCACTGGC	AGGAAAACAG	TTAAAAGAGT	ATGTCGAACT	GCTGCCGGTT
				ACGCCGTTTT
3850	3860	3870	3880	3890
ACCGCCTGTG	TTGGGAGTCA	GGGAAGGTCT	TTAATTACGA	TAACGATCAA
				ACCCGGCTCG
3910	3920	3930	3940	3950
AAGCGCAGAT	TCAGCAGTTT	AATCCCCGCG	ATGTCGAAGG	TTATCGTCAG
				TTTCTGGACT
3970	3980	3990	4000	4010
ATTCACGCGC	GGTGTTTAAA	GAAGGCTATC	TAAAGCTCGG	TACTGTCCCT
				TTTTTATCGT
4030	4040	4050	4060	4070
TCAGAGACAT	GCTTCGCGCC	GCACCTCAAC	TGGCGAAACT	GCAGGCATGG
				AGAAGCGTTT
4090	4100	4110	4120	4130
ACAGTAAGGT	TGCCAGTTAC	ATCGAAGATG	AACATCTGCG	CCAGGCGTTT
				TCTTTCCACT
4150	4160	4170	4180	4190
CGCTGTTGGT	GGGCGGCAAT	CCCTTCGCCA	CCTCATCCAT	TTATACGTTG
				ATACACGCGC
4210	4220	4230	4240	4250
TGGAGCGTGA	GTGGGGCGTC	TGGTTTCCGC	GTGGCGGCAC	CGGCGCATT
				GTTTCAGGGGA
4270	4280	4290	4300	4310
TGATAAAGCT	GTTTCAGGAT	CTGGGTGGCG	AAGTCGTGTT	AAACGCCAGA
				GTCAGCCATA
4330	4340	4350	4360	4370
TGGAAACGAC	AGGAAACAAG	ATTGAAGCCG	TGCATTTAGA	GGACGGTCGC
				AGGTTCTCTGA
4390	4400	4410	4420	4430
CGCAAGCCGT	CGCGTCAAAT	GCAGATGTGG	TTCATACCTA	TCGCGACCTG
				TTAAGCCAGC
4450	4460	4470	4480	4490
ACCCTGCCGC	GGTTAAGCAG	TCCAACAAAC	TGCAGACTAA	GCGCATGAGT
				AACTCTCTGT
4510	4520	4530	4540	4550
TTGTGCTCTA	TTTTGGTTTG	AATCACCATC	ATGATCAGCT	CGCGCATCAC
				ACGGTTTGTT

FIG. 7 (d)

4570	4580	4590	4600	4610
TCGGCCCGCG	TTACCGCGAG	CTGATTGACG	AAATTTTAA	TCATGATGGC
4630	4640	4650	4660	4670
ACTTCTCACT	TTATCTGCAC	GCGCCCTGTG	TCACGGATTC	GTCAGTGGCG
4690	4700	4710	4720	4730
GCGGCAGTTA	CTATGTGTTG	GCGCCGGTGC	CGCATTTAGG	CACCGCGAAC
4750	4760	4770	4780	4790
CGGTTGAGGG	GCCAAACTA	CGCGACCGTA	TTTTTGCGTA	CCTTGAGCAG
4810	4820	4830	4840	4850
CTGGCTTACG	GAGTCAGCTG	GTCACGCACC	GGATGTTTAC	GCCGTTTGAT
4870	4880	4890	4900	4910
AGCTTAATGC	CTATCATGGC	TCAGCCTTTT	CTGTGGAGCC	CGTTCTTACC
4930	4940	4950	4960	4970
GGTTTCGGCC	GCATAACCGC	GATAAAACCA	TTACTAATCT	CTACCTGGTC
4990	5000	5010	5020	5030
CGCATCCCGG	CGCAGGCATT	CCTGGCGTCA	TCGGCTCGGC	AAAAGCGACA
5050	^H 5060	5070	5080	5090
TGCTGGAGGA	TCTGATTGTA	ATAATCCGTC	GTTACTCAAT	CATGCGGTCTG
5110	5120	5130	5140	5150
AGTTGGCTCG	AAAAGTTTTG	CGACAGCCTC	AAAGTTATTT	GATGCAAAAA
5170	5180	5190	5200	5210
CGTACTGATG	CTCTACGCCT	GGTGCCGCCA	TTGTGACGAT	GTTATTGACG
5230	5240	5250	5260	5270
GGGCTTTCAG	GCCCGGCAGC	CTGCCTTACA	AACGCCCGAA	CAACGTCTGA
5290	5300	5310	5320	5330
GATGAAAACG	CGCCAGGCCT	ATGCAGGATC	GCAGATGCAC	GAACCGGCGT
5350	5360	5370	5380	5390
TCAGGAAGTG	GCTATGGCTC	ATGATATCGC	CCCGGCTTAC	GCGTTTGATC
5410	5420	5430	5440	5450
CTTCGCCATG	GATGTACGCG	AAGCGCAATA	CAGCCAACCTG	GATGATACGC
5470	5480	5490	5500	5510
CTATCACGTT	GCAGGCGTTG	TCGGCTTGAT	GATGGCGCAA	ATCATGGGCG
5530	5540	5550	5560	5570
CGCCACGCTG	GACCGCGCCT	GTGACCTTGG	GCTGGCATTG	CAGTTGACCA
5590	5600	5610	5620	5630
CGATATTGTG	GACGATGCGC	ATGCGGGCCG	CTGTTATCTG	CCGGCAAGCT
5650	5660	5670	5680	5690
TGAAGGTCTG	AACAAAGAGA	ATTATGCGGC	ACCTGAAAC	CGTCAGGCGC

FIG. 7 (e)

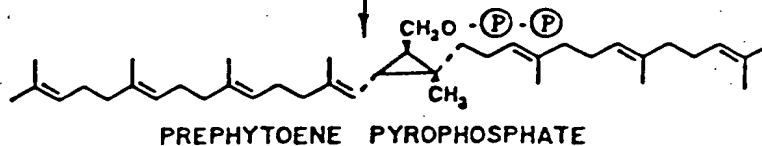
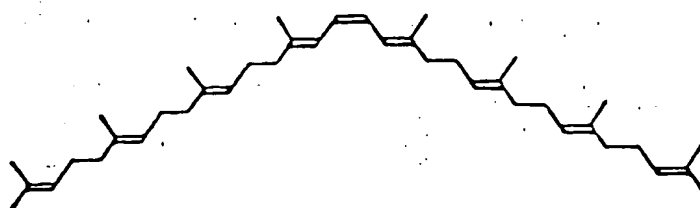
5710 5720 5730 5740 5750
 CGCCCGTCGT TTGGTGCAGG AAGCAGAACC TTACTATTTG TCTGCCACAG CCGGCCTGGC
 5770 5780 5790 5800 5810
 AGGGTTGCCC CTGCGTTCCG CCTGGGCAAT CGCTACGGCG AAGCAGGTTT ACCGGAAAAT
 5830 5840 5850 5860 5870
 AGGTGTCAAA GTTGAACAGG CCGGTCAGCA AGCCTGGGAT CAGCGGCAGT CAACGACCAC
 5890 5900 5910 5920 5930
 GCCCGAAAAA TTAACGCTGC TGCTGGCCGC CTCTGGTCAG GCCCTTACTT CCCGGATGCG
 5950 5960 5970 5980 5990
 GGCTCATCCT CCCC GCCCTG CGCATCTCTG GCAGCGCCCG CTCTAGCGCC ATGTCTTTCC
 6010 6020 6030 6040 6050
 CGGAGCGTCG CCTGAAGTTT TGACAGGGGC GGCGCATAGA GGAAGCCAAA AGAAACACAA
 6070 6080 6090 6100 6110
 CCTTCTTTGC CCCTGACGGC GTGATGCATA CCGTGCGCCA TATACAACCG TTTGAGGTAG
 6130 6140 6150 6160 6170
 CCCTTGCGTG GAATATAGCG GAATGGCCAA CGTTGATGCA CCAGCCCGTC GTGCACCATA
 6190 6200 6210 6220 6230
 AAATAGAGTA ATCCATACGC CGTCATACCT GCGCCAATCC ACTGGAGCGG CCACATTCTT
 6250 6260 6270 6280 6290
 GTACTGCCCA GATAAATCAG CAGGATCGAT AATGCAGCAA AAACCACGGC ATAAAGATCG
 6310 6320 6330 6340 6350
 TTAACCTCAA ACGCACCTTT ACGCGGTTCA TGATGTGAAA GATGCCATCC CCAACCCAG
 6370 6380 6390 6400 6410
 CCGTGCGATGA TGTATTTGTG TGCCAGTGCA GCAATCACTT CCATGCCAAT CACGGTAACG
 6430 6440 6450 6460 6470
 AAAACGATCA GGGCATTCCA AATCCACAAC ATAATTTCTC CGGTAGAGAC GTCTGGCAGC
 6490 6500 6510 6520 6530
 AGGCTTAAGG ATTCAATTTT AACAGAGATT AGCCGATCTG GCGGCGGGAA GGGAAAAAGG
 6550 6560 6570 6580 6590
 CGCGCCAGAA AGGCGCGCCA GGGATCAGAA GTCGGCTTTC AGAACCACAC GGTAGTTGGC
 6610 6620 6630 6640 6650
 TTTACCTGCA CGAACATGGT CCAGTGCATC GTTGATTTTC GACATCGGGA AGTACTCCAC
 6670 6680 6690 6700 6710
 TGTCGGCGCA ATATCTGTAC GGCCAGCCAG CTTGAGCAGT GAACGCAGCT GCGCAGGTGA
 6730 6740 6750 6760 6770
 ACCGGTTGAA GAACCCGTCA CGGCGCGGTC GCCTAAAATC AGGCTGAAAG CCGGGCACGT
 6790 6800 6810 6820 6830
 CAAACGGCTT CAGTACGGCA CCCACGGTAT GGAACCTACC GCGAGGCGCC AGGGCCGCAA

FIG. 7 (f)

6850 6860 6870 6880 6890
AGTAGGGTTG CCAGTCGAGA TCGACGGCGA CCGTGCTGAT AATCAGGTCA AACTGGCCCG
6910 6918
CCAGGCTTTT TAAAGCTT

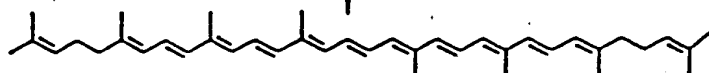
FIG. 7 (g)

DNA SEQUENCE ⑤ (c r t B)

DNA SEQUENCE ① (c r t E)

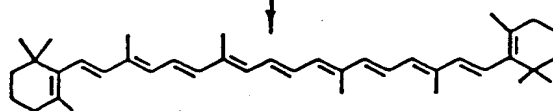
PHYTOENE

DNA SEQUENCE ④ (c r t I)



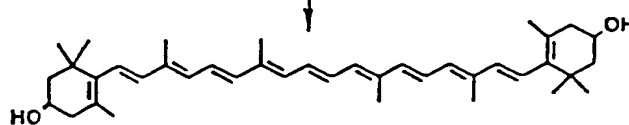
LYCOPENE

DNA SEQUENCE ③ (e r t Y)



β - CAROTENE

DNA SEQUENCE ⑥ (c r t Z)



ZEAXANTHIN

(c r t X)

DNA SEQUENCE

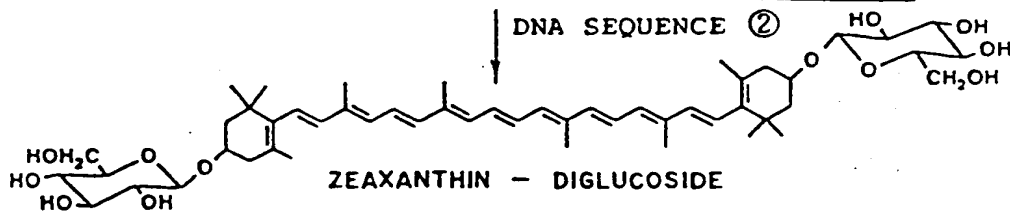


FIG. 8

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